

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 30, 2002, 18:01:01 ; Search time 2325.7 Seconds  
(without alignments)  
3229.042 Million cell updates/sec

Title: US-09-303-518d-649

Perfect score: 4374  
Sequence: 1 atgaaacaacgcagcaacg.....aattagctacgcgtgtaa 4374

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N\_Geneseq\_032802.\*

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23:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4374	100.0	4374	20	AA12251
2	4374	100.0	4374	21	AA12587
3	4374	100.0	4374	21	AA181302
4	4374	100.0	26778	21	AA181477
5	4374	100.0	349980	21	AA12612
6	4374	100.0	837096	21	AA181489
7	4358	99.6	4374	21	AA18918
8	4197.2	96.0	4365	21	AA18917
9	3954.8	90.4	4407	20	AA12253

10	3508	80.2	4350	20	AA12252	Neisseria meningit
11	1467.2	33.5	2991	20	AA12250	Neisseria meningit
12	1249.4	28.6	4319	17	AA17215	Adhesion and penet
13	1128.4	25.8	1312	21	AA181400	N. meningitidis Me
14	883.6	20.2	891	21	AA181401	N. meningitidis Me
15	767.8	17.6	781	21	AA181402	N. meningitidis Me
16	209.8	4.8	959	18	AA188142	H. influenzae Hap
17	196.2	4.5	30078	21	AA181520	N. meningitidis pa
18	196.2	4.5	349980	21	AA121608	Neisseria meningit
19	179	4.1	642	21	AA181729	N. meningitidis pa
20	174.4	4.0	4296	21	AA154326	Neisseria meningit
21	174.4	4.0	16526	21	AA181472	N. meningitidis pa
22	174.4	4.0	172325	21	AA121613	Neisseria meningit
23	174.4	4.0	349980	21	AA121612	Neisseria meningit
24	149	3.4	5091	11	AA181614	The iga gene, enco
25	135	3.1	4113	22	ABA89172	Escherichia coli p
26	135	3.1	48254	22	ABA89141	Escherichia coli p
27	135	3.1	48345	22	ABA89142	Escherichia coli p
28	118.4	2.7	4128	22	ABA88994	Escherichia coli p
29	118.4	2.7	7654	22	ABA88991	Escherichia coli p
30	104.6	2.4	116	21	AA181786	N. meningitidis pa
31	45.8	1.0	10732	21	AA10594	Gene encoding a su
32	45.4	1.0	1859	20	AA125214	Maize ferulate-5-h
33	45.4	1.0	1859	22	AA196683	Maize ferulate-5-h
34	45.2	1.0	4403765	22	AA196683	Maize ferulate-5-h
35	44.4	1.0	4461	23	AB114674	Mycobacterium tube
36	44.4	1.0	1212	21	AA170218	Drosophila melanog
37	44	1.0	1231	21	AA161800	Plasmodium falcipa
38	43.6	1.0	400	19	AA164545	Trichoderma longib
39	43.6	1.0	400	19	AA164545	M. tuberculosis im
40	43.6	1.0	400	20	AA1219346	M. tuberculosis im
41	43.6	1.0	400	20	AA1219346	M. tuberculosis im
42	43.4	1.0	35133	21	AA181518	N. meningitidis an
43	43.4	1.0	349980	21	AA121611	N. meningitidis re
44	43.4	1.0	837096	21	AA181489	Neisseria meningit
45	43	1.0	3489	22	AA130290	N. meningitidis pa
46	43	1.0	3489	22	AA182901	Kaposi's sarcoma-a
47	43	1.0	32207	20	AA173805	Nucleotide sequenc
48	43	1.0	137507	19	AA119941	KSHV LTR DNA (nucl
49	42	1.0	1439	19	AA164533	KSHV Long unique c
50	42	1.0	1439	19	AA164533	M. tuberculosis im
51	42	1.0	1439	20	AA1219334	Mycobacterium tube
52	42	1.0	1439	20	AA1219334	M. tuberculosis an
53	42	1.0	2271	11	AA106844	M. tuberculosis re
54	42	1.0	6741	21	AA110595	Amylase gene from
55	41.8	1.0	4590	22	AA124065	Gene encoding a su
56	41.8	1.0	6365	22	AA117804	Yeast AAD9604-asso
57	41.8	1.0	6365	22	AA117805	Human nervous syst
58	41.8	1.0	58857	21	AA158471	Nucleotide sequenc
59	41.6	1.0	5975	15	AA1055758	Klebsiella pneumon
60	41.4	0.9	2294	18	AA163246	Genomic sequence e
61	41.2	0.9	2716	23	AB115073	Drosophila melanog
62	41	0.9	4403765	22	AA199663	Mycobacterium tube
63	41	0.9	4411529	22	AA199663	Mycobacterium tube
64	40.8	0.9	960	22	AA101504	Codon modified hum
65	40.8	0.9	2068	22	AA198282	Rabbit EST-derived
66	40.8	0.9	2885	23	AB108459	Drosophila melanog
67	40.8	0.9	3848	23	AB108136	Drosophila melanog
68	40.8	0.9	5004	23	AB108458	Drosophila melanog
69	40.6	0.9	1325	22	AA118533	PFUSAB vector DNA
70	40.4	0.9	1412	17	AA126989	Thermus aquaticus
71	40.4	0.9	2291	9	AA180309	Entire amylase gen
72	40.2	0.9	1098	24	AA197227	Neisseria meningit
73	40.2	0.9	4804	21	AA126086	CDNA encoding a re
74	40.2	0.9	4411529	22	AA199682	Mycobacterium tube
75	40	0.9	1957	18	AA193809	An artificial modl
76	40	0.9	4466	21	AA114663	Nucleotide sequenc
77	40	0.9	4478	21	AA114661	Nucleotide sequenc
78	40	0.9	4547	21	AA114664	Nucleotide sequenc
79	40	0.9	4571	21	AA114662	Nucleotide sequenc
80	40	0.9	77536	21	AA114651	Nucleotide sequenc
81	39.8	0.9	1925	21	AA118251	Sphingomonas elode
82	39.6	0.9	12588	15	AA1063293	Sequence encoding



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Qy 1021 aaatcaatgccaacatgaacaaatctctgacctaaatagatataaacaagacgct 1080  
Db 1021 aaatcaatgccaacatgaacaaatctctgacctaaatagatataaacaagacgct 1080  
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Db 1081 caatgtttaatgtttctttatccgagacagcaagaaacggttatcatgtcgaagt 1140  
Qy 1141 ggtgtcaacagttatccgacccagactgaaatggaataatattcctttatgagaa 1200  
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Query Match	100.0%;	Score 4374;	DB 21;	Length 4374;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4374; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

[illegible]

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QY	1081	caatgttcaatggtttcttctacccgagacgcaagaaacccgtttatcatgctcaggt	1140
Db	1081	caatgttcaatggtttcttctacccgagacgcaagaaacccgtttatcatgctcaggt	1140
QY	1141	gggtccaacagttatcgacccagacgtgaataatgtagaataattctcttattgacga	1200
Db	1141	gggtccaacagttatcgacccagacgtgaataatgtagaataattctcttattgacga	1200
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QY	1321	atcagtgtaagcaattaccgttacttggaaagtbaacgcggtggcaaacgacgctgtcc	1380
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QY	1441	gtgggcgacggtacagatcatttggatcagcagcgacgacgataaaggcaaaaacaacgac	1500
Db	1441	gtgggcgacggtacagatcatttggatcagcagcgacgacgataaaggcaaaaacaacgac	1500
QY	1501	tttgatgaataacggtcttggtgcagcgcgacgaggggtacggtgcaatgaatggcggatlaacg	1560
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QY	1621	tcggtcttcgttccacggtatttcaaaataccggttgaaggggcgataattgttaaccacaat	1680
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QY	1681	caagacaaaagaatccacaccttaccatttacaaggcaataaagaatattgtctacaacggcgcat	1740
Db	1681	caagacaaaagaatccacaccttaccatttacaaggcaataaagaatattgtctacaacggcgcat	1740
QY	1741	aaacaacgcttggatattgcaaaaagaataattgcctacaacggttggatttggcgaagaagat	1800
Db	1741	aaacaacgcttggatattgcaaaaagaataattgcctacaacggttggatttggcgaagaagat	1800
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QY	1861	ctgctgcttccggtcggaacaaatttbaaaggcaacatcagcaacgcaaaacgcaaaatg	1920
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QY	2041	aaagcggaanaacttccaattaaaggcggaacgagcggtgttcccgcaatggttgcgcaa	2100
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the present invention describes methods of obtaining immunogenic proteins from *Neisseria* genomic sequences. AAB4143 to AAB42414 represent specifically claimed *Neisseria meningitidis* genomic DNA sequences; AAB41260 to AAB41303 and AAB25620 to AAB25663 represent *Neisseria* DNA sequences and their corresponding proteins; AAB41254 to AAB41259 and AAB41304 to AAB41321 represent PCR primers used in the isolation of *Neisseria meningitidis* DNA sequences; and AAB41322 to AAB41452 represent *Neisseria meningitidis* MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to a *Neisseria* bacteria. For example, some of the identified proteins could be components of vaccines against *Neisseria meningitidis* B, against all serotypes, and/or against all pathogenic *Neisseriae*. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious *Neisseria meningitidis* B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions.

901 cagctggttcglaagattgttctatgatgaatccttgcctgagataccattcagta 960

501 cccacgaaaccacg tcaaaaatgggaaatactcttttaacgacgataataatgacagga 1020



Db 961 ttctaagaccacgiccaaataatgggaatactctttaaagcagataataatgacagga 1020  
QY 1021 aaatacaatgccaacaatgaaacacaaatctctgcttaataagataaaacagacgtt 1080  
Db 1021 aaatacaatgccaacaatgaaacacaaatctctgcttaataagataaaacagacgtt 1080  
QY 1081 caattgttaattgttcttcttaacgagacagaaagaaacctgtttatcatgctgaggt 1140  
Db 1081 caattgttaattgttcttcttaacgagacagaaagaaacctgtttatcatgctgaggt 1140  
QY 1141 ggtgtcaaaagtatccagccagactgaaataatggagaataattcttcttaataagaa 1200  
Db 1141 ggtgtcaaaagtatccagccagactgaaataatggagaataattcttcttaataagaa 1200  
QY 1201 ggaagagcggaattgatacttaacgcaacatcaatcaagtgctgaggaattatctc 1260  
Db 1201 ggaagagcggaattgatacttaacgcaacatcaatcaagtgctgaggaattatctc 1260  
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Db 1261 caagaggaattacggtctcgctgaaataacgaaacttgcaagagcgcgaggttcat 1320  
QY 1321 atcagtgaaagacagtaacgcttacttgaaagtaaaagcggtgagcaaacgagctgtcc 1380  
Db 1321 atcagtgaaagacagtaacgcttacttgaaagtaaaagcggtgagcaaacgagctgtcc 1380  
QY 1381 aaaaatcgcaaaagcgagctgcaagtcgaagccaaaggggaaacccaaggtctgacagc 1440  
Db 1381 aaaaatcgcaaaagcgagctgcaagtcgaagccaaaggggaaacccaaggtctgacagc 1440  
QY 1441 gttggagcaggtgatactatcttggatcagcagcagacgataaagcgcaaaaacagcgc 1500  
Db 1441 gttggagcaggtgatactatcttggatcagcagcagacgataaagcgcaaaaacagcgc 1500  
QY 1501 tttagtgaataatcggtctgtgacagcgaggggtacggtgcaactgaaatgccaataacag 1560  
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QY 1801 acgacccaacgaacggggtgctcaacgtgttaccagcccgcgagagaagcgacac 1860  
Db 1801 acgacccaacgaacggggtgctcaacgtgttaccagcccgcgagagaagcgacac 1860  
QY 1861 ctgctgcttcctcgcggaacaaatttaacggcaacatccagcaaaaacggcaaatg 1920  
Db 1861 ctgctgcttcctcgcggaacaaatttaacggcaacatccagcaaaaacggcaaatg 1920  
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Db 1981 aaagaggggactcctcgcgaggaataatcgtgtggacaacagctgataacacgacatt 2040  
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QY 2101 gttgaagcgatggtgattgagcaatcacgcccagacagttttgtgtcgcacccgat 2160  
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Db 2701 ggcgaatlaaaacttgacaacgcccacatcaactcaacttcgcgctacgcagatgag 2760  
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QY 2881 gtaaacgccaatgtgaacggttcagggaaacatccgcttattgtcggaacttcgctac 2940  
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QY 2941 cgcagcgacaatgtgaagctgaggaaggttccggaagcgacttaaccttgcggtcaac 3000  
Db 2941 cgcagcgacaatgtgaagctgaggaaggttccggaagcgacttaaccttgcggtcaac 3000  
QY 3001 aataccggagcaaaccttcaagcctcgacaacatgtgaagctgaggaagaaagcaac 3060  
Db 3001 aataccggagcaaaccttcaagcctcgacaacatgtgaagctgaggaagaaagcaac 3060  
QY 3061 aaacgcgttcggaacacatcttaacccctgcaaacgaaacgacgctgagtcgagcg 3120  
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QY 3121 tggcgttaccacatctcgcgaagaagcgcgaggttcggtcgtcatatccggttcaagaa 3180  
Db 3121 tggcgttaccacatctcgcgaagaagcgcgaggttcggtcgtcatatccggttcaagaa 3180



[illegible]

Db	4261	ggcgttaaacgcgcgaatcaaaagtttcaagctgtcccttcacagctgcgcgcgaagaagc	4320
Oy	4321	ccgaacatcggaagcgcaacacacgcgggcataatctaggctacgcgtgttaa	4374
Db	4321	ccgaacatcggaagcgcaacacacgcgggcataatctaggctacgcgtgttaa	4374
RESULT 4	AAA81477		
ID	AAA81477	standard; DNA; 26778 BP.	
XX	AAA81477:		
AC	AAA81477:		
XX			
DT	04-DEC-2000	(first entry)	
XX			
DE	N. meningitidis partial DNA sequence gnm_25 SEQ ID NO:25.		
XX			
KW	Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;		
KW	antigen; vaccine; diagnosis; infection; antibacterial; identification;		
XX	Meningococcus B; MenB; ds.		
XX	Neisseria meningitidis.		
OS			
PN	W0200022430-A2.		
XX			
PD	20-APR-2000.		
XX			
PF	08-OCT-1999; 99WO-US23573.		
XX			
PR	09-OCT-1998; 98US-0103794.		
XX			
PI	30-APR-1999; 99US-0132068.		
XX			
PA	(CHIR ) CHIRON CORP.		
PI	Frazier CM, Hickey E, Peterson J, Tettein H, Venter JC;		
PI	Masimani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;		
PI	Rapponi R, Pizzi M;		
XX			
XX	WPI; 2000-318079/27.		
PT			
PT	Isolated nucleotide sequences of Neisseria meningitidis which can be		
PT	used in the diagnosis and treatment of N. meningitidis infection and		
XX	other Neisseria infections, for example, N.gonorrhoea -		
PS	Claim 7; Page 524-531; 1760pp; English.		
XX			
CC	The present invention describes methods of obtaining immunogenic		
CC	proteins from Neisseria genomic sequences. AAA81453 to AAA82414		
CC	represent specifically claimed Neisseria meningitidis genomic DNA		
CC	sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent		
CC	Neisseria DNA sequences and their corresponding proteins; AAA81254 to		
CC	AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the		
CC	isolation of Neisseria meningitidis DNA sequences; and AAA81322 to		
CC	AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF		
CC	sequences, which are all used in the exemplification of the present		
CC	invention. The nucleic acid sequences, protein sequences, and antibodies		
CC	against them, can be used in the manufacture of a composition. The		
CC	composition can be used as a medicament (or in the manufacture of a		
CC	medicament) for treating, preventing or diagnosing infection due to		
CC	Neisseria bacteria. For example, some of the identified proteins could		
CC	be components of vaccines against Meningococcus B; against all serotypes		
CC	and/or against all pathogenic Neisseriae. Identification of sequences		
CC	from the bacterium will also facilitate production of biological probes,		
CC	particularly organism-specific probes. Attempts to make efficacious		
CC	Meningococcus B vaccines have failed mainly due to antigen tolerance.		
CC	Multivalent vaccines have also been tried but none have successfully		
CC	overcome antigenic variability. The provision of further, complete		
CC	sequences may provide an opportunity to identify secreted or surface		
CC	exposed proteins that may be presumed targets for the immune system and		
CC	which are not antigenically variable or at least more conserved than		
XX	other more variable regions.		



QY 2101 gtfaaagcgatgtgcatcttgagcaatcagccgaagcagttttgtgtctgacccgcat 2160  
DB 11945 gtfaaagcgatgtgcatcttgagcaatcagccgaagcagttttgtgtctgacccgcat 12004  
QY 2161 caaagcgacacacatctgtctacogtcttgagctggaagcgtctgcaaatgtgtctgaanaa 2220  
DB 12005 caaagcgacacacatctgtctacogtcttgagctggaagcgtctgcaaatgtgtctgaanaa 12064  
QY 2221 accattaccgaataaagtgtgtcttcatgtactaagaccgaatacagcgcaatgtc 2280  
DB 12065 accattaccgaataaagtgtgtcttcatgtactaagaccgaatacagcgcaatgtc 12124  
QY 2281 gatcttgcgcatcagctcatcttaaatctcagagcgctgtgcacacatcaacgcatctt 2340  
DB 12125 gatcttgcgcatcagctcatcttaaatctcagagcgctgtgcacacatcaacgcatctt 12184  
QY 2341 agtgcgaatgtgcatatcagttatcatcagtcagcaaacgccaacccaaacgccaactt 2400  
DB 12185 agtgcgaatgtgcatatcagttatcatcagtcagcaaacgccaacccaaacgccaactt 12244  
QY 2401 agcctctgtggaatgcccgaagcaacatcttaagccacattaaagcgcaacacatcgc 2460  
DB 12245 agcctctgtggaatgcccgaagcaacatcttaagccacattaaagcgcaacacatcgc 12304  
QY 2461 gcttcggcgcaatgtctcatcttaactcagcgacccagcgctacaaaagcgagcttgagc 2520  
DB 12305 gcttcggcgcaatgtctcatcttaactcagcgacccagcgctacaaaagcgagcttgagc 12364  
QY 2521 ctttcggcgcaacgctaaagcgcaaacgcttaagccatcttcgcaactcaacgtaatgtctcccta 2580  
DB 12365 ctttcggcgcaacgctaaagcgcaaacgcttaagccatcttcgcaactcaacgtaatgtctcccta 12424  
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DB 12425 gccgaataagcgagtaattccatttgaagcgagcgcgcttaccgagcaacataagcgcgcg 12484  
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DB 12485 aaggaataagcgatatacactcttaaaagacagcggaatgtgagcgctgtccgaagcgagaaat 12544  
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QY 3961 gcaagatacgcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 4020  
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Oy	1021	aaatcaatgcocaaactctgaacaaacttcctgcgtaataagattaaacacgcgaacgctt	1080
Db	288171	AAAAATCAATGCTCCAAACATGATMAACAATTCCTGCTTAATGATTTAAAAACAGAACGCTT	288111
Oy	1081	caattgcttaatgttcttcattaccgcggaagaagaagaacccgtttatcatctgctgcagct	1140
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Oy	1141	ggtgtcaacagttatcgcaccgcgaactgtaataatggagaabaatctccctttattgagaa	1200
Db	288051	GGGTCAACAGTTATGACACCCAGACGTGATATGAGAAATATTTCTTTATTAGAGAA	287992
Oy	1201	ggaaaaaggcgaattgtaattaccgcgcaacatcaactaaggctgcgtgaggtattatctc	1260
Db	287991	GGAAAAAGGCAATGTGATCTTACCGACCAACATCATCAAGTGCCTGGAGGATTTATTTTC	287932
Oy	1261	caagagagattttaaagctccgcctcaataaataagaacttggcaagcgcgaggggttcat	1320
Db	287931	CAAGGAGATTTTACGGTCTCGCGCTGAAAATMACAACTTTG6CAAGGCGCGGGGCTTCAT	287872
Oy	1321	atcaatgaaagaacgtacgcttaacttggaaatgaacggtcgtgcgaacgcgcgtctcc	1380
Db	287871	ATCAAGTGAAGACAGTACCGCTTACTTGGAAATGTAAACGGCGTGGCAACGCCCTGTCTC	287812
Oy	1381	aaatctgcgaagggcagcctgtgaagttaaagccaaaggggaaaaacaaagctcgtataagc	1440
Db	287811	AAAAATGCGMAAGGCAACGCTGTGACCTTTCAMCCAAAGGGGMAAACCAAGCCTGATACAG	287752
Oy	1441	gtggcgacgctacagctatcttggatcaagcagcagcaataaaggcaaaaaaacagcc	1500
Db	287751	GTGGCGACAGGTACAGTCAATTTTGGATCAGCAGGCACACGTAAAGGCANAAAAACAGCC	287692
Oy	1501	tttaagtgaatcgtgcttggctgaagcggaagggtacggtgcaactgtaatgcgataacag	1560
Db	287691	TTTATGTAATTCGCTTGCTGTGACGGGACAGGGGTACGGGTGCACATGATGCCATATATCAG	287632
Oy	1561	ttcaaccccgcaacacttatcttgcgcttcgcggcggaagcttggatttaaacygcaat	1620
Db	287631	TTCAACCCCGCAAACTCTATTGGCCTTTCGCGCGAGCGTTTGGATTTAAACGGGCAAT	287572
Oy	1621	tcgcttcgtctccacgctatccaataacagatgaaggcggaatgtaatgtcaacccaat	1680
Db	287571	TCGCTTTCGTTCCACCGTATTCAAAATACGATGAAAGGGCGATGTGTGCAAACCAAT	287512
Oy	1681	caagcacaagaatccacccgtttaccatacgggaagaataagatatgtctacaacggccaat	1740
Db	287511	CAAGCAAAAGATCTCACCGCTTACCATTACAGCAATTAATAATTTCTTCAACCGGCAAT	287452
Oy	1741	aacaaagcttggatagcaaaaaaagaattgtcctaacaagcttggcttggcgaagaagat	1800
Db	287451	AACAACACCTGTGATAGCAAAAAAAGAAATTTGCTACACGCTTGGTTTGGCGAGAAAGAT	287392
Oy	1801	acgaccaaaagaacggggcggtctcaacctgtgtttaccagccgcgcgacagaagacgcaccc	1860
Db	287391	ACGACCAAAAGCAACGGGCGGCTTCACCTTGTTTACACCGCCGCGACAGAACGCGAACCC	287332
Oy	1861	ctgctgccttcccgacggaacaaattttaaaggagaataacgcaaaacaaagcgaactg	1920
Db	287331	CTGCGCTTTCGGCGGGAACAAATTTTAACGGCAATATACCCAAACAAACGGCAAACTG	287272
Oy	1921	tttttcagcggaagaacacacgcgcagccttaacatcatctttaaagacatctgtgctcgaa	1980
Db	287271	TTTTTCAGCGGCAACCAACACCGCGACGCTCAATCATTTTAAAGACATTTGGTCGCA	287212
Oy	1981	aaagagggaacttcctgcgcggggaatccggtggagacaacgactgataccacgcacatt	2040
Db	287211	AAAAGAGGCATTTCTCGCGGGGAAATTCGTGGGACAAAGCATGTGATTAACCGCACATTT	287152
Oy	2041	aaacgcggaacacttccaaattaaaggcggacagcggtgtttccgcgaatggttgcaaa	2100
Db	287151	AAACGGAATAACTTCCAAATTAAGCGGGAACAGCGGTGTGTTTCCCGCAATGTTGCCAAA	287092
Oy	2101	gtgaagaagcgattgagcaatttgagcaatcaagcccaagaagtttggctgcacgcgat	2160

D	287091	GTGAAGGCATTGGCAATTGGACCAATACAGGCCAAGCGATTGTGGTGGCCAGCAT	28703
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D	287031	CAAGGCACACAATCTGTACACGTTGGACTGGACGGGTCTGACAAATTTGTGTCAAAAA	28697
Q	2221	acaaatccagacgaataaagatgattgcttattgactaaagacccgaatacgaagcgaatgc	2280
D	286971	ACCAATTACCAACGATTAAAGTAGTGGTTCAATTGACTTAAGAACCCGACATCAGGGCAATGTC	286912
Q	2281	gattctgcgaatacagctcatcttaaatctcacaaggagctgtgcacactaacggaactct	2340
D	286911	GATCTTGGCATCAGCTCATTTAATATCTCACAGGGCTTGGCACACTCAACGGCAATCTT	28685
Q	2341	atgtcaaatgtggaatacagttatctatcagctcagccaaagccaaacccaaacggaacctt	2400
D	286851	AGTGCAATATGGCAATACAGTTATATACGACACCAACAAAGCCACCAAAAGCGCAACTT	286792
Q	2401	agactcgttgggcaatgcaccaagaacaatttaataagccacatlaaaggaagaacatcg	2460
D	286791	AGCCTCGTGGCAATGCCACAGCAACATTTATATCAAGCCACATTTAAAGGGAACACATTCG	286732
Q	2461	gcttcgggcaatgcttcatttaactcctaagcgaacccagccgtctacaaaagcagctcagc	2520
D	286731	GCTTCGGGCAATGCTTCATTTATATCATGACGCCACCGCGGTACAAAAGCGCAGTCTAGC	286672
Q	2521	cttcgcgcaaacgttaaggaacaaagtaagcaatcccgacaccgaagtaatgtctcccta	2580
D	286671	CTTTCGGGCAACCGTAAAGCAACCTTAAGCCATTCGACATCAAGGTAAATGTTCTCCCTA	286612
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Q	2641	aaggaataagcgaatcaactaaagaacagcggaatggaacgctgtccgttaaggacggaatta	2700
D	286551	AAGGATACGGCATTTACACTTAAAMACAGCGCAATTAAGACGGCTGCGTACGACAGGAATTA	286492
Q	2701	ggcaatttaaaccttgacacgcgaacgtcaacatlaactcaatccgcctatcgcacagatgcg	2760
D	286491	GGCAATTTAAACCTTGACCAAGCCGCCATTTACACTCAATTCGCGTATGCGCCAGATGCG	286432
Q	2761	ggaaggagcgcaaacgcggaagtgcacagatgctgcgcgcgcgcgcgttcgcgcgttcgcgc	2820
D	286431	GCAGGGGCGCAACCGGCAAGTGCACAGATGCGCGCGCGCGCTTCGCCCTTGCGCGC	286372
Q	2821	cgctccctatlaatccgtttacacgcgcgaacttcggtgaatcccggttcaaacgcgcgaag	2880
D	286371	CGTTCCTTATTATCGGTACACGCCCAACTTCGGTAAATATCCGTTTCACACAGCGTGAAG	286312
Q	2881	gtaaacggcgaatgtgaacggttcagggaacatccgccttatgttcggaactcttcgctac	2940
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Q	2941	gcgaacgcgaatgtgaacgtgcgggaagaagttccgaagacacttaacactttgcgcgtcaac	3000
D	286251	CGCACCGCAATTTGAAGCTTGGCGGAAGTTCCGAAGGCACTTACACTTTGGCGGTCAAC	286192
Q	3001	aataccggaacgaacactgcaagcgttcgaacaaatltgaagtlagtgaagaagaagaacac	3060
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[illegible]

OY 4321 ccggaactggaagcgcacacacagcgccgggcatcaatattaggtaccgcctggtta 4374  
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 ID AAA81489/c  
 AC AAA81489 standard; DNA; 837096 BP.  
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 AC  
 XX AAA81489;  
 DT 04-DEC-2000 (first entry)  
 XX  
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 KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;  
 KW antigen; vaccine; diagnosis; infection; antibacterial; Identification;  
 KW Meningococcus B; MenB; ds.  
 XX  
 XX Neisseria meningitidis.  
 OS  
 PN WO200022430-A2.  
 XX  
 PD 20-APR-2000.  
 XX  
 PF 08-OCT-1999; 99WO-US23573.  
 XX  
 PR 09-OCT-1998; 98US-0103794.  
 PR 30-APR-1999; 99US-0132068.  
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 XX (CHIR ) CHIRON CORP.  
 XX  
 PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;  
 PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;  
 PI Rappuoli R, Pizza M;  
 XX  
 DR WPI: 2000-318079/27.  
 XX  
 PT Isolated nucleotide sequences of Neisseria meningitidis which can be  
 PT used in the diagnosis and treatment of N. meningitidis infection and  
 PT other Neisserial infections, for example, N.gonorrhoea -  
 XX  
 Claim 7; Page 629-865; 1760pp: English.  
 XX  
 PS  
 XX  
 XX The present invention describes methods of obtaining immunogenic  
 CC proteins from Neisseria genomic sequences. AAA81453 to AAA82414  
 CC represent specifically claimed Neisseria meningitidis genomic DNA  
 CC sequences. AAA81260 to AAA81303 and AAB25620 to AAB25663 represent  
 CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to  
 CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the  
 CC isolation of Neisseria meningitidis DNA sequences; and AAA81322 to  
 CC AAA814453 represent Neisseria meningitidis MenB polynucleotide ORF  
 CC sequences, which are all used in the exemplification of the present  
 CC invention. The nucleic acid sequences, protein sequences, and antibodies  
 CC against them, can be used in the manufacture of a composition. The  
 CC composition can be used as a medicament (or in the manufacture of a  
 CC medicament) for treating, preventing or diagnosing infection due to  
 CC Neisserial bacteria. For example, some of the identified proteins could  
 CC be components of vaccines against Meningococcus B; against all serotypes  
 CC and/or against all pathogenic Neisseriae. Identification of sequences  
 CC from the bacterium will also facilitate production of biological probes,  
 CC particularly organism-specific probes. Attempts to make efficacious  
 CC Meningococcus B vaccines have failed mainly due to antigen tolerance.  
 CC Multivalent vaccines have also been tried but none have successfully  
 CC overcome antigenic variability. The provision of further, complete  
 CC sequences may provide an opportunity to identify secreted or surface  
 CC exposed proteins that may be presumed targets for the immune system and  
 CC which are not antigenically variable or at least more conserved than  
 CC other more variable regions.  
 XX  
 XX Sequence 837096 BP; 207534 A; 227065 C; 205215 G; 197280 T; 2 other;  
 SQ







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Sequence 4374 BP; 1269 A; 1158 C; 1066 G; 881 T; 0 other

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 QY 3481 ctgcaaccccaacgcgcaaccccaacgcgcaacgcgcaacgcgcaacgcgcaacgc 3540  
 DB 3481 ctgcaaccccaacgcgcaaccccaacgcgcaacgcgcaacgcgcaacgcgcaacgc 3540  
 QY 3541 ggttgagtgaaatttcgcgacgctcaacagcggttcgcgtaacagcggaattagc 3600  
 DB 3541 ggttgagtgaaatttcgcgacgctcaacagcggttcgcgtaacagcggaattagc 3600  
 QY 3601 cgcgtatttcgcaagacgcgcgcaacgcggttcgcaacgcgcaacgcgcaacgc 3660  
 DB 3601 cgcgtatttcgcaagacgcgcgcaacgcggttcgcaacgcgcaacgcgcaacgc 3660  
 QY 3661 cactacggttcgcaagatcttcgcgctacacgcgcaacacacgcgctgcgaacgcgt 3720  
 DB 3661 cactacggttcgcaagatcttcgcgctacacgcgcaacacacgcgctgcgaacgcgt 3720  
 QY 3721 atgcaaaaaaacctcgc 3780  
 DB 3721 atgcaaaaaaacctcgc 3780  
 QY 3781 aacacgttcgcaacgc 3840  
 DB 3781 aacacgttcgcaacgc 3840  
 QY 3841 caatacgc 3900  
 DB 3841 caatacgc 3900  
 QY 3901 agccttcgaacgc 3960  
 DB 3901 agccttcgaacgc 3960  
 QY 3961 gcaagatacgc 4020  
 DB 3961 gcaagatacgc 4020  
 QY 4021 tattcgtccaaaacgcgattacgcgtacgaaacgtaaatatccgccccgcgcgcgc 4080  
 DB 4021 tattcgtccaaaacgcgattacgcgtacgaaacgtaaatatccgccccgcgcgcgc 4080  
 QY 4081 gcatcaacgc 4140  
 DB 4081 gcatcaacgc 4140  
 QY 4141 attcacaacgc 4200  
 DB 4141 attcacaacgc 4200  
 QY 4201 aacgcggttaataacgc 4260  
 DB 4201 aacgcggttaataacgc 4260  
 QY 4261 ggcgttaaacgc 4320  
 DB 4261 ggcgttaaacgc 4320

QY 4321 ccgcaacttgaagcgcacaacacgc 4374  
 DB 4321 ccgcaacttgaagcgcacaacacgc 4374

## RESULT 8

AAZ38917 standard; DNA; 4365 BP.

AAZ38917;

21-FEB-2000 (first entry)

Neisseria meningitidis strain ATCC13090 BASB006 nucleotide sequence.

Neisseria meningitidis; BASB006; diagnosis; bacterial; infection;

vaccine; antibiotic; upper respiratory tract infection; meningitis;

invasive bacterial disease; bacteraemia; screening; antibacterial; ss.

Neisseria meningitidis.

Key Location/Qualifiers

1..4365

20-APR-1999; 99NO-EP02766.

24-APR-1998; 98GB-0008866.

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

Thomnard J;

WPI: 2000-052810/04.

P-PSDB: AAY56621.

Novel polynucleotides and polypeptides from *Neisseria meningitidis* used to prepare vaccines against bacterial infections

Claim 11: Page 84-86; 103pp; English.

The present sequence encodes BASB006 isolated from *Neisseria meningitidis* strain ATCC13090. BASB006 polynucleotides and polypeptides may be employed as research reagents and material for the discovery of treatments and diagnostics for diseases, particularly human diseases. They can be used for diagnosis of disease, staging of disease, or determining response of an infectious organism to drugs. The polynucleotides may be used as a source for hybridisation probes, and for screening of genetic mutations, serotype, organism or strain identification, identification of mutation in BASB013 sequences, and as components of arrays which are useful for diagnostic and prognostic purposes. The polypeptides can be used to produce antibodies. The polypeptides can also be used in vaccine formulations, and to identify agonists and antagonists. The polypeptides, antibodies, agonists and antagonists (which are bacteriostatic) are used for the treatment and prevention of diseases such as upper respiratory tract infection, invasive bacterial diseases such as bacteraemia and meningitis, and for the development and screening of antibacterial drugs. They are also used on in-dwelling devices, or to extracellular matrix proteins used to prevent tissue damage and/or block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

Sequence 4365 BP; 1267 A; 1149 C; 1066 G; 883 T; 0 other;

Query Match 96.0%; Score 4197.2; DB 21: Length 4365;



QY	2161	caagcgacacacatctgtacacggttcgagctggaacgggttcgacaaattgtcgcgaaaa	2220
Db	2161	caaaagccacacatctgttacaacgttcgcgactggacgggtctgcaaatgtgtcgaaaaa	2220
QY	2221	accattccagacataaagtgtgtgttcctcatgtgtaagccgacatcagcggcaatgtc	2280
Db	2221	accattacgcagacataaagtgtgtgttcctcatgtgtaagccgacatcagcggcaatgtc	2280
QY	2281	gacctgtgcgatacgcgttcatttaaatctccaaagggttcgcacacatcaagcgcaatt	2340
Db	2281	agccttgcgatacgcgttcatttaaatctccaaagggttcgcacacatcaagcgcaatt	2340
QY	2341	agtcgcaaatgtgcgatacgcgtttatacagtgacgcaaaagccaaacggcgcaacct	2400
Db	2341	agtcgcaaatgtgcgatacgcgtttatacagtgacgcaaaacggcgcaacct	2400
QY	2401	agccttcgttggcgaaatgcccgaagcaacatttaataagccacattaaagcgcaacacg	2460
Db	2401	agccttcgttggcgaaatgcccgaagcaacatttaataagccacattaaagcgcaacacg	2460
QY	2461	gctcggcgaaatgctctcaatttaacttaacgagccacgcgctgataaaacggcgatcagc	2520
Db	2461	gctcggcgaaatgctctcaatttaacttaacgagcaacgcgctgataaaacggcgatcagc	2520
QY	2521	ctttccggaacagcctaagcgcaaaagctaaagcattccgcacataaaggttaagtctccta	2580
Db	2521	ctttccggaacagcctaagcgcaaaagctaaagcattccgcacataaaggttaagtctccta	2580
QY	2581	gccggttaagcgagatcttcacatttgaaagcagcgcttaccgcgcaaatcagcggcgc	2640
Db	2581	gccggttaagcgagatcttcacatttgaaagcgagcgcttaccgcgcaaatcagcggcgc	2640
QY	2641	aaggaataagcgatatacacttaaaagacagagaaatgagcgtgcgctaaagcgagta	2700
Db	2641	aaggaataagcgatatacacttaaaagacagagaaatgagcgtgcgctaaagcgagta	2700
QY	2701	ggcaatttaaacctcttgacaaagccacacatataactaaattccgcctatcgcacagatgc	2760
Db	2701	ggcaatttaaacctcttgacaaagccacacatataactaaattccgcctatcgcacagatgc	2760
QY	2761	ggaaggcgcaaaacggcgcaatgagagaagtgccgcgcgcgcgttcgcgcgttcgcgc	2820
Db	2761	ggaaggcgcaaaacggcgcaatgagagaagtgccgcgcgcgcgttcgcgcgttcgcgc	2820
QY	2821	cgcttcctataatccggttataccgcgcaacatttggtagatcccgcttcaacaacgcgtgaag	2880
Db	2821	cgcttcctataatccggttataccgcgcaacatttggtagatcccgcttcaacaacgcgtgaag	2880
QY	2881	gtaaacggcaaatgtgaacgcgttcaggggaataattccgcttattgtcugaaactcttcgctac	2940
Db	2881	gtaaacggcaaatgtgaacgcgttcaggggaataattccgcttattgtcugaaactcttcgctac	2940
QY	2941	cgcaagcgcaaatgtgaagcgttcgagcaaaagtctccgaagcatttaccacttcggcggttcaac	3000
Db	2941	cgcaagcgcaaatgtgaagcgttcgagcaaaagtctccgaagcatttaccacttcggcggttcaac	3000
QY	3001	aataccggaacgaacacttcgaagcctcgacaacatttgacgctagtgtgaagaaagaacaac	3060
Db	2992	aataccggaacgaacacttcgaagcctcgacaacatttgacgctagtgtgaagaaagaacaac	3051
QY	3061	aaacgcgcttcggaaaaccttaatttcaacccctgcgaacgaacgcttgatctcgcgcg	3120
Db	3052	aaacgcgcttcggaaaaccttaatttcaacccctgcgaacgaacgcttgatctcgcgcg	3111
QY	3121	tgaggttacaacatactccgcaaaagacggcgagttccgcctgcataatccggttcaagaa	3180
Db	3112	tgaggttacaacatactccgcaaaagacggcgagttccgcctgcataatccggttcaagaa	3171
QY	3181	caagagcttccgacaaactcggcaagcgcaaaagccaaaaaacaagcggaaaaagaacac	3240
Db	3172	caagagcttccgacaaactcggcaagcgcaaaagccaaaaaacaagcggaaaaagaacac	3231

[illegible]

|||||  
Db 4312 ccgaactggagcgcaacacagcgcgatcaatagctacgcgtgta 4365

## RESULT 9

AA12253 standard; DNA; 4407 BP.

AA12253;

08-OCT-1999 (first entry)

Neisseria gonorrhoeae complete ORF1 sequence.

Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

treatment; Neisseria infection; meningitis; septicemia; gonorrhea; ss.

Neisseria gonorrhoeae.

W0924578-A2.

20-MAY-1999.

09-OCT-1998; 98WO-IB01665.

01-SEP-1998; 98GB-0019016.

06-NOV-1997; 97GB-0023516.

14-NOV-1997; 97GB-0024190.

27-NOV-1997; 97GB-0024386.

10-DEC-1997; 97GB-0025158.

14-JAN-1998; 97GB-0026147.

14-JAN-1998; 98GB-0000759.

(CHIR-) CHIRON SPA.

Grandi G, Maignani V, Piza M, Rappulli R, Scarlato V.

WPI: 1999-327407/27.

P-PSDB; AAY38825.

Proteins from Neisseria meningitidis and N. gonorrhoeae useful for

diagnosis, treatment and prevention of infection

Claim 9; Page 370-371; 524pp; English.

Nucleotide sequences AA11972-212358 represent open reading frames

(ORFs) of Neisseria meningitidis and N. gonorrhoeae which encode

antigenic proteins (see AAY38499-Y38944). The antigenic proteins, their

fragments, their nucleic acids and antibodies are used for diagnosis,

prevention (as vaccines) or treatment of Neisseria infections,

such as meningitis, septicemia and gonorrhea. Both organisms

are closely related. Fragments of the nucleic acids are useful

as hybridisation probes and antisense reagents.

Sequence 4407 BP; 1273 A; 1169 C; 1094 G; 871 T; 0 other;

Query Match 90.4%; Score 3954.8; DB 20; Length 4407;

Best Local Similarity 94.0%; P-DB: 0; Mismatches 212; Indels 51; Gaps 2;

Matches 4153; Conservative 0; Mismatches 212; Indels 51; Gaps 2;

181 aaagcgcaatttcagtcgagcgcaagaatattgagtttacaacaaaaggagttg 240  
181 aaagcgcaatttcagtcgagcgaggaagattgagtttacaacaaaaggagttg 240  
241 gtcgcaaatcaatgacaaaagcccgatgatttctgtgtgtgtgtgtgtgtgtgt 300  
241 gtcgcaaatcaatgacaaaagcccgatgatttctgtgtgtgtgtgtgtgtgtgt 300  
301 gtcgcaaatcaatgacaaaagcccgatgatttctgtgtgtgtgtgtgtgtgtgt 360  
301 gtcgcaaatcaatgacaaaagcccgatgatttctgtgtgtgtgtgtgtgtgtgt 360  
361 aacgtgatttgggtgcggaaggaagaaatcccgatcaacatcgttttcttataat 420  
361 aacgtgatttgggtgcggaaggaagaaatcccgatcaacatcgttttcttataat 420  
421 gtcgcaaatcaatgacaaaagcccgatgatttctgtgtgtgtgtgtgtgtgtgt 480  
421 gtcgcaaatcaatgacaaaagcccgatgatttctgtgtgtgtgtgtgtgtgtgt 480  
481 atgcggtttgcatataattgtcacagatgcagaaactgttgaaatgacagattatg 540  
481 atgcggtttgcatataattgtcacagatgcagaaactgttgaaatgacagattatg 540  
541 gatggcggaatatatcgaatcaaatatcaccctgacgtgtgtgtgtgtgtgtgtgt 600  
541 gatggcggaatatatcgaatcaaatatcaccctgacgtgtgtgtgtgtgtgtgtgt 600  
601 aggcgaatttggcgatcgtggaagatgaggaagcaataacgcggaagttatcatat 660  
601 aggcgaatttggcgatcgtggaagatgaggaagcaataacgcggaagttatcatat 660  
661 agacataatgagcgatcgtggaagatgaggaagcaataacgcggaagttatcatat 660  
661 agacataatgagcgatcgtggaagatgaggaagcaataacgcggaagttatcatat 660  
720 gcaagtcgatttctgt 720  
720 gcaagtcgatttctgt 720  
721 ggcacagtcacatttgcgtggaagatgaggaagcaataacgcggaagttatcatat 780  
721 ggcacagtcacatttgcgtggaagatgaggaagcaataacgcggaagttatcatat 780  
781 ggcagtcacatttgcgtggaagatgaggaagcaataacgcggaagttatcatat 840  
781 ggcagtcacatttgcgtggaagatgaggaagcaataacgcggaagttatcatat 840  
841 tggtaattatgaggt 900  
841 tggtaattatgaggt 900  
901 cagctgt 960  
901 cagctgt 960  
961 tttacgaacacagtcgaatgaggaatcttcttaacgagatgaataatgaggaag 1020  
961 tttacgaacacagtcgaatgaggaatcttcttaacgagatgaataatgaggaag 1020  
1021 aaatacagtcgaatgaggaatcttcttaacgagatgaataatgaggaag 1080  
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1081 caattgttattgttcttattatcgcagacagcaaggaacgtttatcatatgtcaggt 1140  
1081 caattgttattgttcttattatcgcagacagcaaggaacgtttatcatatgtcaggt 1140  
1141 ggtgtcaacagtcac 1200  
1141 ggtgtcaacagtcac 1200  
1201 ggaagagcgaattgtgacttaccagcaacatcaacaggtgtgtgtgtgtgtgtgtgt 1260  
1201 ggaagagcgaattgtgacttaccagcaacatcaacaggtgtgtgtgtgtgtgtgtgt 1260  
1261 caagagatttaccgt 1320



Db 1261 gagggaattttacggtctcgcgttaaaaaacagaaacggtgcaaggcgcggttcatt 1320  
QY 1321 atcagtgagaagatgacggttaacttggaagtaaacggtgagcaacgacggtctcc 1380  
Db 1321 atcagtgagaagatgacggttaacttggaagtaaacggtgagcaacgacggtctcc 1380  
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QY 1441 gtaggagcaggtacagtcattttgatatcagcagcagcaaaagcaaaagcgc 1500  
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Db 1501 tttatgaaatccggttgtagcagcagcaggtgtagcgtgcaatgacggtatcag 1560  
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Db 1621 tgcgttcgttcacggttattcaaaatcagcagtgaaagggcagtgatgtcaaccacaa 1680  
QY 1681 caagacaagaatccacggttaccatcagcagcaataaagatatgtctcaacggtcag 1740  
Db 1681 caagacaagaatccacggttaccatcagcagcaataaagatatgtctcaacggtcag 1740  
QY 1741 aacaaagcgttgtagttagcaaaaagaattgctcacaacggttggtttgagcaagaag 1800  
Db 1741 aacaaagcgttgtagttagcaaaaagaattgctcacaacggttggtttgagcaagaag 1800  
QY 1801 acgacccaacacgaaacgagcggtcacaactgtttaccagcccgcaagaacggtcagc 1860  
Db 1801 gcaacccaacacgaaacgagcggtcacaactgtttaccagcccgcaagaacggtcagc 1860  
QY 1861 ctggtgtttccggtcggaacaaatttaaacgcaacatcagcaacaaacggtcagc 1920  
Db 1861 ctggtgtttccggtcggaacaaatttaaacgcaacatcagcaacaaacggtcagc 1920  
QY 1921 ttttcggtcggtcagcaacacggtcagcaacatcatttaacgacatggttcagaa 1980  
Db 1921 ttttcggtcggtcagcaacacggtcagcaacatcatttaacgacatggttcagaa 1980  
QY 1981 aaagaggggcatctcctcggtggaatcgtgtggaacaaacggtgacacggtcatt 2040  
Db 1981 atggaaggtatcccaacaaagaaatcgtgtggaacaaacggtgacacggtcatt 2040  
QY 2041 aaagcggaacacgttcaaaattaaagcggtcagcaggtggttccgcaatgttcagaa 2100  
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Db 2101 gtagaagcggtatggtcatttgacaatcagcagcagcaggttttgggttcgacggat 2160  
QY 2161 caaagcacaacacgttgcacaggttcgagcgggttcgacaatgtgttcgaaaaa 2220  
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QY 2341 atgcaaatggtgacacgttattacgttgcacaaacggtcagcagcagcagcagcagc 2400  
Db 2341 atgcaaatggtgacacgttattacgttgcacaaacggtcagcagcagcagcagcagc 2400

Db 2341 atgcaagcggtgacacggttatacgttgcagcagcagcagcagcagcagcagc 2400  
QY 2401 agcctcgttgggaatggtcccaagcaacatttaacagcagcagcagcagcagcagc 2460  
Db 2401 agcctcgttgggaatggtcccaagcaacatttaacagcagcagcagcagcagcagc 2460  
QY 2461 gcttcggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2520  
Db 2461 gcttcggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2520  
QY 2521 ctcttcggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2580  
Db 2521 ctcttcggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2580  
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QY 2701 ggcatttaaaccttgcagcagcagcagcagcagcagcagcagcagcagcagcagc 2760  
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QY 2761 gcaagggcgcaaaacggtcagcagcagcagcagcagcagcagcagcagcagcagc 2820  
Db 2761 gcaagggcgcaaaacggtcagcagcagcagcagcagcagcagcagcagcagcagc 2820  
QY 2821 ggttccttatttcgttgcagcagcagcagcagcagcagcagcagcagcagcagcagc 2880  
Db 2821 ggttccttatttcgttgcagcagcagcagcagcagcagcagcagcagcagcagcagc 2880  
QY 2881 gtaaacggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2940  
Db 2881 gtaaacggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2940  
QY 2941 gtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2991  
Db 2941 gtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2991  
QY 3001 aatacggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3060  
Db 3001 aatacggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3060  
QY 3061 aaacggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3120  
Db 3061 aaacggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3120  
QY 3121 tggcgttaccacacgttgcagcagcagcagcagcagcagcagcagcagcagcagcagc 3180  
Db 3121 tggcgttaccacacgttgcagcagcagcagcagcagcagcagcagcagcagcagcagc 3180  
QY 3181 caagagcgttcgcaaaactcggcaagcgagaa----- 3240  
Db 3181 caagagcgttcgcaaaactcggcaagcgagaa----- 3240  
QY 3241 -----gcaaaaaacagcggtgcaaaacagcagcagcagcagcagcagcagcagc 3300  
Db 3241 -----gcaaaaaacagcggtgcaaaacagcagcagcagcagcagcagcagcagc 3300  
QY 3301 ctggttgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3360  
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QY 3361 gtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3420  
Db 3361 gtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3420  
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Db 3421 gtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3480



QY 361 aacgttgatttggcggaagaagaatcccgatcaacatcggtttactataaatt 420  
DB 361 aacgttgatttggcggaagaagaatcccgatcaacatcggtttactataaatt 420  
QY 421 gtgaaagcgaataataataaagcaggaactaaagccatctatgycggcgattatc 480  
DB 421 gtgaaagcgaataataataaagcaggaactaaagccatctatgycggcgattatc 480  
QY 481 atgcgcgtttgataaattgtcacagatgagaacccgttgaaatgacagattatg 540  
DB 478 atgcgcgtttgataaattgtcacagatgagaacccgttgaaatgacagattatg 537  
QY 541 gatgagcgaataataataaataaataaataaataaataaataaataaataaataa 600  
DB 538 agggggaataaataaataaataaataaataaataaataaataaataaataaataa 597  
QY 601 aggcataattgagcagatgaaatgagccataacccgaaagtcatcatatt 660  
DB 598 caccactattgagcagatgaaatgagccataacccgaaagtcatcatatt 651  
QY 661 gcaagtgcgtatcttgcgttcgttgcaataccttgcaaaatgagtcagtggt 720  
DB 652 gca-----tgtaattgycgcaataacatacagaggttggggaataat 699  
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DB 700 ggcacagcaacttggatgtaaaaaataaataaataaataaataaataaataaataa 759  
QY 781 ggaagcatttggcgaagtgccacaaatgttacttcttggccaaagcaaaag 840  
DB 760 ggaagcatttggcgaagtgccacaaatgttacttcttggccaaagcaaaag 819  
QY 841 tggtaataatgaggtatgcaaaagcgaacccataataggaataaagcaatggttc 900  
DB 820 tggtaataatgaggtatgcaaaagcgaacccataataggaataaagcaatggttc 879  
QY 901 cagctggttcgtaagaatggttctatgataaattcttctgagatgaccatcagta 960  
DB 880 cagctggttcgtaagaatggttctatgataaattcttctgagatgaccatcagta 939  
QY 961 ttctacgaacacgtcaaaatggaataactctttaaagcagataaataatgacagaa 1020  
DB 940 ttctacgaacacgtcaaaatggaataactctttaaagcagataaataatgacagaa 999  
QY 1021 aaaaatgcgaacacgtcaaaatggaataactcttctgataatgataaataaagcagtt 1080  
DB 1000 aaaaatgcgaacacgtcaaaatggaataactcttctgataatgataaataaagcagtt 1056  
QY 1081 caattgttaattgttcttatacgaagcagaaagacccgttataatgctgagtt 1140  
DB 1057 cgaactgttgagcaactcttgaatgaaactgataaagaacagattc--acgcggaag 1113  
QY 1141 ggttcaacaggtatcgacccagacgtgaataatggaataaataatcttctttaaagca 1200  
DB 1114 ggttcaacaggtatcgacccagacgtgaataatggaataaataatcttctttaaagca 1173  
QY 1201 ggaataagcgaatgataacttaccagcaacatcaatcaaggtgctggagagattatctc 1260  
DB 1174 ggaataagcgaatgataacttaccagcaacatcaatcaaggtgctggagagattatctc 1233  
QY 1261 caaggaatcttgcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttc 1320  
DB 1234 gaaggttatttgcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttc 1293  
QY 1321 atcagtaagaagcagtaacttacttggaaatgaaacgcgttggcaacgcgcgttc 1380  
DB 1294 atcagtaagaagcagtaacttacttggaaatgaaacgcgttggcaacgcgcgttc 1353  
QY 1381 aaaaatgcgaacacgttcgacgttcaagcgaaggggaataaagcgaacgcgttc 1440  
DB 1354 aaaaatgcgaacacgttcgacgttcaagcgaaggggaataaagcgaacgcgttc 1413

QY 1441 gtggcgacgtaacagtaacttggatcagcagcgacagataaagcgaataaagcc 1500  
DB 1414 gtggcgacgtaacagtaacttggatcagcagcgacagataaagcgaataaagcc 1473  
QY 1501 ttatgtaaatcggttcgttcagcagcggttacggttcaactaatgacataatg 1560  
DB 1474 ttatgtaaatcggttcgttcagcagcggttacggttcaactaatgacataatg 1533  
QY 1561 ttaaccccgacaatactcatttgcgttcgttcgttcgttcgttcgttcgttcgttcgttc 1620  
DB 1534 ttaaccccgacaatactcatttgcgttcgttcgttcgttcgttcgttcgttcgttcgttc 1593  
QY 1621 tgcgttcgttcacccgataaataaataaataaataaataaataaataaataaataa 1680  
DB 1594 tgcgttcgttcacccgataaataaataaataaataaataaataaataaataaataa 1653  
QY 1681 caagacaagatccacggttaccattacagcgaataaagatgctacaacgcgc-- 1737  
DB 1654 gcaacacaacatccacggttaccattacagcgaataaagatgctacaacgcgc-- 1713  
QY 1738 ---ataacaacagcttgatagcaaaaaaagaatgtgctacacggttggcgag 1794  
DB 1714 aagaatataatgacttaattatagcagaagaataatgctacacggttggcgag 1773  
QY 1795 aagaatataatgacttaattatagcagaagaataatgctacacggttggcgag 1854  
DB 1774 aagaatataatgacttaattatagcagaagaataatgctacacggttggcgag 1833  
QY 1855 cgcacccgttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttc 1914  
DB 1834 cgcacccgttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttc 1893  
QY 1915 aaactggttcttcagcagcagacacacacgcgcgttaccataatgataaagcagcttgg 1974  
DB 1894 aaactggttcttcagcagcagacacacacgcgcgttaccataatgataaagcagcttgg 1953  
QY 1975 tgcgaataaaggggacattccctcgcggggaatctgtggggaacagcgtgataacgcgc 2034  
DB 1954 tgcgaataaaggggacattccctcgcggggaatctgtggggaacagcgtgataacgcgc 2013  
QY 2035 acatttgaagcgaataacttccaaatgaagcgaagcagctgttcccgcaatgtt 2094  
DB 2014 acgtttaaagcgaataacttccaaatgaagcgaagcagctgttcccgcaatgtt 2073  
QY 2095 gccaagtggaagcagcttgcgttgaagcgaacacgcgcagcttgggtgcga 2154  
DB 2074 gccaagtggaagcagcttgcgttgaagcgaacacgcgcagcttgggtgcga 2133  
QY 2155 ccgcatcaagccac 2214  
DB 2134 ccgcatcaagccac 2193  
QY 2215 gaaaaaacattac 2274  
DB 2194 gaaaaaacattac 2253  
QY 2275 aatgcatcttgcgatacgttataatcttcaacagcgttgcacacacacacacacacac 2334  
DB 2254 aatgcatcttgcgatacgttataatcttcaacagcgttgcacacacacacacacacac 2313  
QY 2335 aatcttgaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaat 2394  
DB 2314 aatcttgaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaat 2373  
QY 2395 aacttgaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaat 2454  
DB 2374 aacttgaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatgcaat 2433  
QY 2455 aactggttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttc 2514  
DB 2434 aactggttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttcgttc 2493  
QY 2515 ctgacgcttccgcaacgctaaagcgaacgttaagcgaatccgcgactcaacgttaatgctc 2574





Db 1315 ----- 1314  
QY 1497 agcctttagtaaatcgctgtgcagcgaggggtacggtgcaactgatacgataa 1556  
Db 1315 ----- 1314  
QY 1557 tcagttcaaccccgcaaaactctatttcggtcttcgscgagcggtttgatttaacgg 1616  
Db 1315 ----- 1314  
QY 1617 gcatcgtcttctccacccgtatcaataacgataagggcgatgtgtcaacca 1676  
Db 1315 ----- 1314  
QY 1677 caatacaagaagatccacccgtatcaatcaagcaataaagatatgtctacaacgg 1736  
Db 1315 ----- 1314  
QY 1737 caatacaacagcttggatagcaaaaaaagaaattgcttacaacggttggcttgcgagaa 1796  
Db 1315 ----- 1314  
QY 1797 agatagcaacaaacgaacggcggtcgaacctgtttacagcccgcgagagaagccg 1856  
Db 1315 ----- 1314  
QY 1857 caacctgtgtcttcgscgagcaaaatlttaacgcaacatcagcaaaacagcgcaa 1916  
Db 1315 ----- 1314  
QY 1917 actgttttcaagcgagacaaacacgcgcgtacataatlttaaacgaccttggctc 1976  
Db 1315 ----- 1314  
QY 1977 gcaaaaagagggtatctctcgcgaggaaatcgtgtggagcaacgactggatcaacggcac 2036  
Db 1315 ----- 1314  
QY 2037 atttaagcggaacttccaaatlaaaggcgagacgsgtggtttcccggaatgttgc 2096  
Db 1315 ----- 1314  
QY 2097 caaagtgaagggatgtgcatttgagcaatcagcccaagcagatttgggtgcgcacc 2156  
Db 1315 ----- 1314  
QY 2157 gcatcaaaagccacaaactctgtacaagttcggacttgcgaggtcttgacdaatgtgtcga 2216  
Db 1315 ----- 1314  
QY 2217 aaaaacattacgcagacataaagtgtgttcatgtactaagaccgacatcagcgagca 2276  
Db 1315 ----- 1314  
QY 2277 tgtcagcttgcgcatcagcgtcaatlaaactccacagggcttgcacactcaacggca 2336  
Db 1362 tgtcagcttgcgcatcagcgtcaatlaaactccacagggcttgcacactcaacggca 1421  
QY 2337 tcttagtgcaaatggtcgatcacggttatagctagccacagccaccccaaaacggca 2396  
Db 1422 tcttagtgcaaatggtcgatcacggttatagctagccacagccaccccaaaacggca 1481  
QY 2397 ccttagcctctggcgcaatgccaagcaacatttaacgaacacattaaacggcaacac 2456  
Db 1482 ccttagcctctggcgcaatgccaagcaacatttaacgaacacattaaacggcaacac 1541  
QY 2457 atcggcttcgggcaatgtctcatatttaacgaacacacgcgttacaacacggcggtt 2516  
Db 1542 atcggcttcgggcaatgtctcatatttaacgaacacacgcgttacaacacggcggtt 1601  
QY 2517 gacgtttccggcaacggttaagcaaaagtaagcattccgcaactcaacggtatgtctc 2576

Db 1602 gacgtttccggcaacggttaagcaaaagtaagcattccgcaactcaacggtatgtctc 1661  
QY 2577 ccttagcgataaagcaatatttcaatttgaagcagccgcttaccggaacaaatcagcg 2636  
Db 1662 ccttagcgataaagcaatatttcaatttgaagcagccgcttaccggaacaaatcagcg 1721  
QY 2637 cggcaagatacgcgcatctacacattaaagaacagcgaaatgagcgtgcgtcaagcagga 2696  
Db 1722 cggcaagatacgcgcatctacacattaaagaacagcgaaatgagcgtgcgtcaagcagga 1781  
QY 2697 attagcaatttaaaccttgcacacgacacacattacacacattccgcatatcgacga 2756  
Db 1782 attagcaatttaaaccttgcacacgacacacattacacacattccgcatatcgacga 1841  
QY 2757 tgcgcaagggcgcaaacgcgacgtgcgacagatgcgcgcgcgcgcgcgcgcgcgcgc 2816  
Db 1842 tgcgcaagggcgcaaacgcgacgtgcgacagatgcgcgcgcgcgcgcgcgcgcgcgc 1901  
QY 2817 ggcgcgttcccttataatccgttacaacgcgcacacttgcgttgaatccggttcaacagct 2876  
Db 1902 ggcgcgttcccttataatccgttacaacgcgcacacttgcgttgaatccggttcaacagct 1961  
QY 2877 gacggtlaaacggcaaatlgaaacggtcgaagacacatccgcttattgtcgaactctcgg 2936  
Db 1962 gacggtlaaacggcaaatlgaaacggtcgaagacacatccgcttattgtcgaactctcgg 2021  
QY 2937 ctacccgacgacaaattgaaagctgcggaaggttccgaagacacattccgcttattgtcga 2996  
Db 2022 ctacccgacgacaaattgaaagctgcggaaggttccgaagacacattccgcttattgtcga 2081  
QY 2997 caacaaatccggcaaacggaacgttcgaagcctcgaacacatttgcggttagtggaagaaaga 3056  
Db 2082 caacaaatccggcaaacggaacgttcgaagcctcgaacacatttgcggttagtggaagaaaga 2141  
QY 3057 caacaaacgcgttcgcgaacacatttcaacccctgcgaacacacacacacacacacac 3116  
Db 2142 caacaaacgcgttcgcgaacacatttcaacccctgcgaacacacacacacacacacac 2201  
QY 3117 cgcgtgcgttaccacactatccgcaagacggtcgcgcgtcgcgtcgcgtcgcgtcgc 3176  
Db 2202 cgcgtgcgttaccacactatccgcaagacggtcgcgcgtcgcgtcgcgtcgcgtcgc 2207  
QY 3177 agacaagaagcttccgcaacacactcgcgaagcgaagacacacacacacacacacac 3236  
Db 2208 ----- 2207  
QY 3237 caacgcgcaaacgcttgcagcgtctgattgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 3296  
Db 2208 ----- 2207  
QY 3297 aagcgttgcgcgaacgc 3356  
Db 2208 ----- 2207  
QY 3357 ggaagagaaaaaacggttgcagcgcgaataaagacacgcgcgttcgcgaacacgcgcgaac 3416  
Db 2208 ----- 2207  
QY 3417 ggaacccgcgcgcgttaccacgcgcgttcccccgcgcgcgcgcgcgcgcgcgcgcgcgc 3476  
Db 2208 ----- 2207  
QY 3477 gcaactgcaaccccaacgc 3536  
Db 2208 ----- 2207  
QY 3537 tagcgtttagtgatatttccgcgaacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 3596  
Db 2208 ----- 2212  
QY 3597 agacgcgttatttgcgaagacgc 3656  
Db 2213 agacgcgttatttgcgaagacgc 2272

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QY 3657 caaacactacggttcgcaagatttcgagctacacgcaaaacacgacctgagccaat 3716
DB 2273 caaacactacggttcgcaagatttcgagctacacgcaaaacacgacctgagccaat 2332
QY 3717 cgtatcagaaaaaacctcgcagcgcgctgcgcctcctccttccttcgcaaacggac 3776
DB 2333 cgtatcagaaaaaacctcgcagcgcgctgcgcctcctccttccttcgcaaacggac 2392
QY 3777 cgaataacaccttcgagcagcgttcgcaaacctcgcagcgctgcgcctcctccttc 3836
DB 2393 cgaataacaccttcgagcagcgttcgcaaacctcgcagcgctgcgcctcctccttc 2452
QY 3837 cggagcaatacgcagcagcgttcgcaaacctcgcagcgctgcgcctcctccttc 3895
DB 2453 cggagcaatacgcagcagcgttcgcaaacctcgcagcgctgcgcctcctccttc 2512
QY 3896 ggcggcgaccttcgagcagcgttcgcaaacctcgcagcgctgcgcctcctccttc 3955
DB 2513 ggcggcgaccttcgagcagcgttcgcaaacctcgcagcgctgcgcctcctccttc 2572
QY 3956 ttcagacagatacgcagcagcgttcgcaaacctcgcagcgctgcgcctcctccttc 4015
DB 2573 ttcagacagatacgcagcagcgttcgcaaacctcgcagcgctgcgcctcctccttc 2632
QY 4016 cgcgcatttcgcaaacgagatttcgcaaacctcgcagcgctgcgcctcctccttc 4075
DB 2633 cgcgcatttcgcaaacgagatttcgcaaacctcgcagcgctgcgcctcctccttc 2692
QY 4076 gcttcgcaaacgagatttcgcaaacctcgcagcgctgcgcctcctccttc 4135
DB 2693 gcttcgcaaacgagatttcgcaaacctcgcagcgctgcgcctcctccttc 2752
QY 4136 aacacatttcgcaaacgagatttcgcaaacctcgcagcgctgcgcctcctccttc 4195
DB 2753 aacacatttcgcaaacgagatttcgcaaacctcgcagcgctgcgcctcctccttc 2812
QY 4196 tccgacagcagcagcagcgttcgcaaacctcgcagcgctgcgcctcctccttc 4255
DB 2813 tccgacagcagcagcagcgttcgcaaacctcgcagcgctgcgcctcctccttc 2872
QY 4256 aatggcgagcagcagcagcgttcgcaaacctcgcagcgctgcgcctcctccttc 4315
DB 2873 aatggcgagcagcagcagcgttcgcaaacctcgcagcgctgcgcctcctccttc 2932
QY 4316 aagcccgagcagcagcagcgttcgcaaacctcgcagcgctgcgcctcctccttc 4374
DB 2933 aagcccgagcagcagcagcgttcgcaaacctcgcagcgctgcgcctcctccttc 2991

RESULT 12
AAT17215
ID AAT17215 standard; DNA: 4319 BP.
XX
AC AAT17215;
XX
DT 01-JUN-1996 (first entry)
XX
DE Adhesion and penetration protein gene.
XX
KW Adhesion and penetration protein; hap gene; promoter; terminator;
KW inverted repeat; stem-loop; protease; outer membrane protein;
KW beta-domain; secretion; recombinant vaccine; monoclonal antibody;
KW diagnostic; immunosay; ds.
XX
OS Haemophilus influenzae.
XX
XX
Key Location/Qualifiers
FH -35_signal 5..10
FT /tag= a
FT -10_signal 26..31
FT /tag= b
FT sig_peptide 60..134
```

```
FT FT CDS /tag= c
FT FT 60..4244
FT FT /tag= d
FT FT /product= Adhesion and penetration preprotein
FT FT 135..4241
FT FT /tag= e
FT FT /product= Adhesion and penetration protein
FT FT 135..2936
FT FT /tag= f
FT FT /product= Secreted 110-kDa protease fragment
FT FT 2937..4241
FT FT /tag= g
FT FT /product= 45-kDa outer membrane protein fragment
FT FT 4284..4302
FT FT /tag= h
FT FT repeat_region 4284..4302
FT FT /tag= i
FT FT stem_loop /rpt_type= INVERTED
FT FT 4284..4302
FT FT /tag= j

WO9605858-A1.
XX
XX 29-FEB-1996.
XX
XX 16-AUG-1995; 95WO-US10661.
XX
XX 25-AUG-1994; 94US-0296791.
XX
XX (STRD ) UNIV LELAND STANFORD JUNIOR.
XX (UNIW ) UNIV WASHINGTON.
XX
PI Falkow S, St Geme JW;
XX
XX WPI: 1996-151147/15.
XX
XX P-PSDB: AAR92768.
XX
XX Haemophilus adhesion and penetration protein and corresponding DNA
XX - used to produce vaccines against H. influenzae infection
XX
XX Claim 5; Fig 6; 105bp; English.
XX
XX The sequence encodes a Haemophilus influenzae adhesion and
XX penetration protein. The sequence (hap gene) includes putative
XX -10 and -30 sequences and a putative rho-independent terminator 3'
XX to the hap stop codon. The terminator contains interrupted
XX inverted repeats, with the potential for forming a hairpin
XX structure containing a loop of 3 bases and a stem of 8 bases,
XX followed by a stretch rich in T residues. The gene product is
XX first synthesised as a preprotein, which is transported to the
XX periplasm, followed by insertion of the C-terminal beta-domain into
XX the outer membrane, possibly forming a pore, and export of the
XX N-terminal fragment through the outer membrane, followed by
XX autolysosomal cleavage and secretion of the mature protease, leaving
XX an outer membrane protein fragment. The gene may be inserted in a
XX vector and expressed in recombinant host cells, for use as a
XX diagnostic monoclonal antibody production.
XX
XX Sequence 4319 BP; 1497 A; 776 C; 891 G; 1155 T; 0 other;

Query Match 28.6%; Score 1249.4; DB 17; Length 4319;
Best Local Similarity 58.8%; Pred. No. 0;
Matches 2565; Conservative 0; Mismatches 1536; Indels 264; Gaps 13;

QY 73 cctgctacttgccatgctcgttcgcaatttcgcaaacgctgagcgagac 132
DB 81 ctttaattttaaaccgctgcatctcattagagatagatcgcaagcgtgagcgac 140
QY 133 acttattcgcaataacacatcatcagcagcgttcgcaaacgaggaagttc 192
DB 141 acttattcgcaataacacatcatcagcagcgttcgcaaacgaggaagttc 200
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[illegible]



QY 1199 aaggaagcggaattgatactaccagcaatcatcaatgaagctctggaattatatt 1258  
 Db 1110 aaggaagcggaattgatactaccagcaatcatcaatgaagctctggaattatatt 1169  
 QY 1259 tccaaggaatttcaagctcgcctggaataaacaagaacttggcaagcgcggttc 1318  
 Db 1170 tccaaggaatttcaagctcgcctggaataaacaagaacttggcaagcgcggttc 1229  
 QY 1319 atacagtaagacagctaccgttacttggaaagtaagcgctggcaagcgcctgt 1378  
 Db 1230 atacagtaagacagctaccgttacttggaaagtaagcgctggcaagcgcctgt 1289  
 QY 1379 ccaaatcggaagcgcaagctg 1401  
 Db 1290 ccaaatcggaagcgcaagctg 1312

RESULT 14  
 AAA81401  
 ID AAA81401 standard; DNA; 891 BP.  
 AC AAA81401;  
 DT 04-DEC-2000 (first entry)  
 DE N. meningitidis MenB internal polynucleotide sequence ORF number 76.  
 XX  
 KM Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;  
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;  
 XX Meningococcus B; MenB; ds.  
 OS Neisseria meningitidis.  
 XX  
 PN WO200022430-A2.  
 PD 20-APR-2000.  
 XX  
 PF 08-OCT-1999; 99WO-US23573.  
 XX  
 PR 09-OCT-1998; 98US-0103794.  
 PR 30-APR-1999; 99US-0132068.  
 XX  
 PA (CHIR) CHIRON CORP.  
 XX  
 PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;  
 PI Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;  
 PI Rappunli R, Pizsa M;  
 XX  
 DR WPI: 2000-318079/27.  
 XX  
 PT Isolated nucleotide sequences of Neisseria meningitidis which can be  
 PT used in the diagnosis and treatment of N. meningitidis infection and  
 PT other Neisseria infections, for example, N. gonorrhoea -  
 XX  
 PS Disclosure; Page 219; 1760pp; English.  
 XX  
 CC The present invention describes methods of obtaining immunogenic  
 CC proteins from Neisseria genomic sequences. AAA81453 to AAA82414  
 CC represent specifically claimed Neisseria meningitidis genomic DNA  
 CC sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent  
 CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to  
 CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the  
 CC isolation of Neisseria meningitidis DNA sequences; and AAA81322 to  
 CC AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF  
 CC sequences, which are all used in the exemplification of the present  
 CC invention. The nucleic acid sequences, protein sequences, and antibodies  
 CC against them, can be used in the manufacture of a composition. The  
 CC composition can be used as a medicament (or in the manufacture of a  
 CC medicament) for treating, preventing or diagnosing infection due to  
 CC Neisseria bacteria. For example, some of the identified proteins could  
 CC be components of vaccines against Meningococcus B; against all serotypes;  
 CC and/or against all pathogenic Neisseriae. Identification of sequences  
 CC from the bacterium will also facilitate production of biological probes,

CC particularly organism-specific probes. Attempts to make efficacious  
 CC Meningococcus B vaccines have failed mainly due to antigen tolerance.  
 CC Multivalent vaccines have also been tried but none have successfully  
 CC overcome antigenic variability. The provision of further, complete  
 CC sequences may provide an opportunity to identify secreted or surface  
 CC exposed proteins that may be presumed targets for the immune system and  
 CC which are not antigenically variable or at least more conserved than  
 CC other more variable regions.  
 XX  
 SQ Sequence 891 BP; 255 A; 258 C; 202 G; 171 T; 5 other;

Query Match 20.2%; Score 883.6; DB 21; Length 891;  
 Best Local Similarity 99.1%; Pred. No. 4.1e-245;  
 Matches 883; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2233 gataagtgatgtcttacttacttaagaacgacatcagcggaatgtgacttgcgat 2292  
 Db 1 gataagtgatgtcttacttacttaagaacgacatcagcggaatgtgacttgcgat 60  
 QY 2293 cagctcatttaaatctacagaggttgcacacacacacacacacacacacacacacac 2352  
 Db 61 cagctcatttaaatctacagaggttgcacacacacacacacacacacacacacacac 120  
 QY 2353 gatacagttatagtcagtcacacacacacacacacacacacacacacacacacac 2412  
 Db 121 gatacagttatagtcagtcacacacacacacacacacacacacacacacacacac 180  
 QY 2413 aatgcac 2472  
 Db 181 aatgcac 240  
 QY 2473 gcttcatttaactaagcagacacacacacacacacacacacacacacacacacac 2532  
 Db 241 gcttcatttaactaagcagacacacacacacacacacacacacacacacacacac 300  
 QY 2533 gctaagcacaacgtaagcacttcgacacacacacacacacacacacacacacacac 2592  
 Db 301 gctaagcacaacgtaagcacttcgacacacacacacacacacacacacacacacac 360  
 QY 2593 gtattcatttgaagaac 2652  
 Db 361 gtattcatttgaagaac 420  
 QY 2653 ttaacttaaaagacagcgaatgagcgtgcgtcagcagcgaatgagcgaatgagcga 2712  
 Db 421 ttaacttaaaagacagcgaatgagcgtgcgtcagcagcgaatgagcgaatgagcga 480  
 QY 2713 ctgacaacgac 2772  
 Db 481 ctgacaacgac 540  
 QY 2773 accggaagtgcagacagatgcgcgcgcgttcgcgcgcgttcgcgcgcgttcgcgcga 2832  
 Db 541 accggaagtgcagacagatgcgcgcgcgttcgcgcgcgttcgcgcgcgttcgcgcga 600  
 QY 2833 tccgttacacgcgcac 2892  
 Db 601 tccgttacacgcgcac 660  
 QY 2893 ttgaacgctcaggaac 2952  
 Db 661 ttgaacgctcaggaac 720  
 QY 2953 ttgaacgctcaggaac 3012  
 Db 721 ttgaacgctcaggaac 780  
 QY 3013 gaacctcgaagcctcgaac 3072  
 Db 781 gaacctcgaagcctcgaac 840  
 QY 3073 gaaacaccttaattcacaccttcgacacacacacacacacacacacacacacacacac 3123





Claim 7; Page 1411-1420; 1760pp; English.

The present invention describes methods of obtaining immunogenic proteins from *Neisseria* genomic sequences. AAB21453 to AAB22414 represent specifically claimed *Neisseria meningitidis* genomic DNA sequences; AAB81260 to AAB81303 and AAB25620 to AAB2663 represent *Neisseria* DNA sequences and their corresponding proteins; AAB81254 to AAB81259 and AAB81304 to AAB81321 represent PCR primers used in the isolation of *Neisseria meningitidis* DNA sequences; and AAB81322 to AAB81452 represent *Neisseria meningitidis* MspI polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to *Neisseria* bacteria. For example, some of the identified proteins could be components of vaccines against *Neisseria*. Identification of sequences and/or against all pathogenic *Neisseria*. Identification of biological probes, particularly organism-specific probes. Attempts to make efficacious *Neisseria* meningitidis B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions.

Sequence 30078 BP; 6365 A; 7264 C; 8488 G; 7960 T; 1 other;

Query Match 4.5%; Score 196.2; DB 21; Length 30078;

Best Local Similarity 57.7%; Pred No. 5.9e-45; Indels 3; Gaps 1;

Matches 370; Conservative 0; Mismatches 268;

1198 gaagaaagcgaatgatactactaccagaacatcaatcaagctgagagatataat 1257  
2236 GAAACACAGCGCACTTGGATGATGATCAAAACATCAACAGCGCGGCTGTCTT 22177  
1258 ttccaaagagatttaccgctcgcctgaaataacgaa---actggcaagcgcgggc 1314  
22176 TTCAAGAGCGCATTTACACAGTCAAGATTAATTAATGACATCTCTGGCTAGGCGGG 22117  
1315 gtccatcagcgaagcagctacgttacttgaagaagtaagcgctggcaacgacgc 1374  
22116 ATGATGTTCCGACGCGCAAAAAGTCTGTGGCAAGTCAAAAATCCGAATGCGACAGA 22057  
1375 ctgtccaaatcgcaagcagcgtgcacgttcaagcagaaggggaaacaaagctcg 1434  
22056 TTGGCAAAAATCGCAAGAGCGCATTTGAATTAACGCGCACAGCGCTTAACCAAGGCAA 21997  
1435 atcagcgtggcgagcgttaccgatttggatcagcagcagacataaagcaaaaa 1494  
21996 TTAAATTCGCGCGAGGTAGCGTTATCTGAATCAACACCGATGCGCCCAAAAAAGTGC 21937  
1495 caagcctttagtgaatcagcgttgcacgagcgagcggtlccactgaaatgcccgaat 1554  
21936 CAGGCTTTCGCCAAGTCCGATTTGTCAGGAGCGGTCATTTGATTAATAGTTCA 21877  
1555 aatcagttcaaccccgcaaacactatctcggttctcgggcgagcgttggattaaac 1614  
21876 AATCAGATTAAATCCGATTAATCTTATTTCCGTTCCGTTCCGTTCCGTTCCGTTCCGAT 21817  
1615 gggcattcgttctgtccaccgfatccaaataacatcagatgaagggagatgattcaac 1674  
21816 GGCATGACTTGTCTTTGAAACATCCGCACTGATGAAGCGCGCCGATTTGTCAAC 21757  
1675 cacaatcaagaacaagaatcacccgttaccatcagcagcaataaagatattgtctaac 1734  
21756 CACAACACAGGCGCAAGCGCTGCACAATCAACGCTTAACGGTAAATCTTTGATTACGATCC 21697  
1735 ggcataaacaacagcttgatagcaaaaaaagaatgtcctcaacggttggttgcgag 1794

DB 21696 AATACATCTCTATTCATTATATTAATAATGATGATGAGATGCTGTTATAGTAT 21637  
QY 1795 aaagatacagcaaacagcagcggtcaccactgttta 1835  
DB 21636 TACCGGCTTAGGAACCGATTCACAAAGCGCAAGATCTTTA 21596

RESULT 18

AAP21608/C  
ID AAP21608 standard; DNA: 349980 BP.

AAFP21608;

13-MAR-2001 (first entry)

*Neisseria meningitidis* B nucleotide sequence SEQ ID NO:109.

*Neisseria meningitidis*; *Neisseria gonorrhoeae*; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial;

ds.

*Neisseria meningitidis*.

W0200066791-A1.

09-NOV-2000.

08-MAR-2000; 2000WO-US05928.

30-APR-1999; 99US-0132068.

08-OCT-1999; 99WO-US23573.

28-FEB-2000; 2000GB-0004695.

(CHIRON) CHIRON CORP.

(GENO-) INST GENOMIC RES.

Pizza M, Hickey E, Peterson J, Nettelin H, Venter JC, Maignani V;

Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V, Rappuoli R;

Frazer CM, Grandi G;

WPI; 2000-647603/62.

Neisseria meningitidis B full length genome sequence and open reading

frames are used to detect, treat and prevent *Neisseria* infections -

Claim 7; Appendix A; 692pp; English.

The present invention describes the full length genome of *Neisseria meningitidis* B (NMB). The sequences in AAP21544 and AAP21607 to AAP21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which overlap each other at the beginning and end of each sequence by 49980 bp (i.e. the last 49980 bp of AAP21544 is repeated at the beginning of AAP21607, and so on). AAP21545 to AAP21588 encode the *Neisseria* proteins given in AAB58550 to AAB58593, and AAP21589 to AAP21606 represent PCR primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity. The NMB genome and fragments which binds to the *Neisseria* nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to *Neisseria* bacteria or as a diagnostic reagent for detecting the presence of *Neisseria* bacteria or of antibodies raised to *Neisseria* bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently used.

Sequence 349980 BP; 82523 A; 82940 C; 96712 G; 87805 T; 0 other;



Query Match 4.58; Score 196.2; DB 21; Length 34980;  
 Best Local Similarity 57.7%; Pred. No. 2.9e-44;  
 Matches 370; Conservative 0; Mismatches 268; Indels 3; Gaps 1;

QY 1198 gaaggaagaagcgaattgatactaccagcaacatcaatcaagtcgtgagatattat 1257  
 Db 130038 GAAACAACGCGACTTGGTATTGATCAAAACATACCAACGCGGCGTCTGTTT 129979  
 QY 1258 ttcaagaagatttttcggtcgcctgaataacgaa---acttgcaagcgcgagc 1314  
 Db 129978 TTCAAAAGCGATTACACAGTCAAAAGGTAAATATATGATCATCTGCTAGTGGGG 129919  
 QY 1315 gtccatatacgtgaagacagcttacttggaagtaagcggtgcaacgagcgc 1374  
 Db 129918 ATTGATGTTGCGACGCGCAAAAAGTCGTTGGCAAGTAAATCCGATGCGCAGCA 129859  
 QY 1375 ctgtcacaatctgcgaagaagcgcgtgcgttcaagccaaagggaacccaagctcg 1434  
 Db 129858 TTGGCAAAAATCGGCAAAAGCGCATATGAAATAAACGCGACAGCGGTTAACCAAGCGCA 129799  
 QY 1435 atcagcgtggcgagcgtacagctacatttgatcgacgcgagcagataaagcaaaaa 1494  
 Db 129798 TTAAGAATGCGCGACGCTACGCTTATTCTGAATCAACAAGCGATGCCGACAAAAGTTC 129739  
 QY 1495 caagccttaagtgaatcgcttgcagcgagcgaggtacggtgcaactgaatcgcat 1554  
 Db 129738 CAGCGCTTCTCCCAAGTCGCGCATGTGTCAGCGGACCGGTACATTGCTTAAATATGTTCA 129679  
 QY 1555 aatcaatcaaccggcaacaaactatatttgcttgcggcgagcgtttgatttaac 1614  
 Db 129678 AATCAGATTAAATCCGATATCTATATTTCCGTTTCCCTGCGGCTGCTGATGATGCCAAT 129619  
 QY 1615 gggcattcgcttgcgtccacagctatcaataaccagtgagggcgatgatgttaac 1674  
 Db 129618 GGCATATGACTTGTGGAACATCCGCAACGTGATGATGAGCGCGCATGTGTCAAC 129559  
 QY 1675 ccaatcaagaagaagaatcaacgcttaccattacaggaataaagattgttacaac 1734  
 Db 129558 CACAAACACAGCGCGCTCCACATCAATCAACGCTAACGGGTAAATGTTGATTACGATCCC 129499  
 QY 1735 ggcataacaacagcttgcataagcaaaaagaattgcctacaacgcttggttggag 1794  
 Db 129498 AAAACCATCTCATTTATTAATTCATAAATATGATGATGATGATGATGATGATGAT 129439  
 QY 1795 aagatagaccacaaagcaagcgcgctcaacctgttta 1835  
 Db 129438 TACCGCCTTAGGAAACGATTCACAAAGCAAAAGATCTTTA 129398

RESULT 19  
 AAA81729  
 ID AAA81729 standard; DNA: 642 BP.  
 XX  
 AC AAA81729;  
 DT 04-DEC-2000 (first entry)  
 XX  
 DE N. meningitidis partial DNA sequence gnm\_276 SEQ ID NO: 276;  
 XX  
 KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;  
 XX antigen; vaccine; diagnosis; infection; antibacterial; identification;  
 XX Meningococcus B; MenB; ds.  
 XX  
 OS Neisseria meningitidis.  
 XX  
 PN MO200022430-A2.  
 PD 20-APR-2000.  
 XX  
 PF 08-OCT-1999; 99WO-US23573.  
 XX  
 PR 09-OCT-1998; 98US-0103794.

PR 30-APR-1999; 99US-0132068.  
 XX  
 PA (CHIR) CHIRON CORP.  
 XX  
 PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;  
 PI Meisigant V, Galeotti C, Mora M, Ratti G, Scarselli M, Scariato V;  
 PI Rappelli R, Pizzo M;  
 XX  
 DR WPL: 2000-318079/27.  
 XX  
 PT Isolated nucleotide sequences of Neisseria meningitidis which can be  
 PT used in the diagnosis and treatment of N. meningitidis infection and  
 PT other Neisserial infections, for example, N. gonorrhoea -  
 XX  
 PS Claim 7: Page 1554-1555; 1760pp; English.

The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neisseriae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successful sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions.

Sequence 642 BP; 131 A; 145 C; 193 G; 173 T; 0 other;

Query Match 4.18; Score 179; DB 21; Length 642;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-41;  
 Matches 179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1614 cggcgattcgcttgcgtccacgctatccaataaccagatgaaggcgatgtgtcaa 1673  
 Db 464 cggcgattcgcttgcgtccacgctatccaataaccagatgaaggcgatgtgtcaa 1673  
 QY 1674 ccacaatcaagaagaatccacgcttaccattacaggaagaagaatgtgtgtcaac 1733  
 Db 524 ccacaatcaagaagaatccacgcttaccattacaggaagaagaatgtgtgtcaac 1733  
 QY 1734 cggcaataaacaacagcttgcataagcaaaaagaattgcctacaacgcttggttggag 1792  
 Db 584 cggcaataaacaacagcttgcataagcaaaaagaattgcctacaacgcttggttggag 1792

RESULT 20  
 AA254326  
 ID AA254326 standard; DNA: 4296 BP.  
 XX  
 AC AA254326;  
 DT 21-MAR-2000 (first entry)  
 XX  
 DE Neisseria meningitidis ORF 759 partial DNA sequence SEQ ID NO:2601.  
 XX  
 KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;  
antibacterial; gene therapy; ds.  
Neisseria meningitidis.  
W0957280-A2.  
11-NOV-1999.  
30-APR-1999; 99WO-US09346.  
01-MAY-1998; 98US-0083758.  
31-JUL-1998; 98US-0094869.  
02-SEP-1998; 98US-0098994.  
02-SEP-1998; 98US-0099062.  
09-OCT-1998; 98US-0103749.  
09-OCT-1998; 98US-0103794.  
09-OCT-1998; 98US-0103796.  
25-FEB-1999; 99US-0121528.  
(CHIR) CHIRON CORP.  
(GENO-) INST GENOMIC RES.  
Fraser C, Galeotti C, Grandi G, Hickey E, Maignani V, Mora M;  
Peterson J, Piza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;  
Tettelin H, Venter JC;  
WPI: 2000-062150/05.  
P-PsDB: AAY75564.

Novel Neisserial polypeptides predicted to be useful antigens for  
vaccines and diagnostics  
Claim 7: Page 1232-1234; 1453pp; English.  
AA253015 to AA25436, AA254577 to AA254615, and AAY74253 to AAY75941  
represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides  
and polypeptides. AA254577 to AA254576 and AA254616 to AA25473 represent  
PCR primers used in the exemplification of the present invention. The  
polypeptides, the polynucleotides, antibodies and compositions of  
the invention can be used as vaccines, as diagnostic reagents, and as  
immunogenic compositions. The polypeptides can be used in the  
manufacture of medicaments for treating or preventing infection due to  
Neisserial bacteria (e.g. meningitis and septicemia), to detect the  
presence of Neisseria bacteria, or to raise antibodies. They may also  
be used to screen for agonists or antagonists, which may themselves  
have use as antibacterial agents. The polynucleotides of the invention  
may also be used in gene therapy protocols.

Sequence 4236 BP; 1192 A; 1470 C; 959 G; 675 T; 0 other;  
Query Match 4.08; Score 174.4; DB 21; Length 4236;  
Best Local Similarity 60.3%; Pred. No. 3,4e-39;  
Matches 305; Conservative 0; Mismatches 196; Indels 3; Gaps 1;

1212 attatattacacgaacatcaagaagtctgtgagaattatattccaaaggagatt 1271  
1074 actgatctgtgcagacacatatacaacgaagcgagcgttcgafttcagacgaact 1133  
1272 tacgtctcgcctgaataaactgaagaagcgcggttcattatcagtgaaaga 1331  
1134 caccgtc---gtcggtlaaaacacacattgcaaggtgcaggttactcgttagccgaag 1190  
1332 cagtcctcttacttggaagaactgaagaagcggtgcagcgcctgtccaaactcgcaaa 1391  
1191 caacgcgtctcttgcgaagtcaggaacccaaagcgagcgttcctccaaactggcgaa 1250  
1392 aggcacgtgcagcttcaagcaaggaaggaacccaagcgtcgtcgttggcgagcg 1451  
1251 aggcacgtctatcgcaacgagcaagcatcaacgaggtgcacatcgcgtggggaag 1310  
1452 tacagtcattttgatcgcagcgacgaagataaagcaaaacgaagcctttagtgaat 1511

1311 cactgtgtactcgcgcacaaagctcttcacagcgagcaacaaagcattcaacaaagt 1370  
1512 cggcttgtaagcgagcgaggtacgtgcacatgcgcgttaacatcaccocga 1571  
1371 cggcatcacacagcgagcgagcgagcggtcctccgcgcgaacgacgaatacaacocga 1430  
1572 caactcatttgcgttcgcgcgcagcgttgcatttaaacgagcattcgttgc 1631  
1431 aaactcatttgcgttcgcgcgcagcgttcgcgcgcgaactcaacgaacacttcctt 1490  
1632 caacgtatcaaaataccgatgaagggcgatgatgttcaacacaaatcaagcaaga 1691  
1491 taccataatccgcagtcgagcgagcgagcaatcgtatcaacacacttgacaaagc 1550  
1692 atccacgttaccattcaagcga 1715  
1551 cggacactgaagcgttcagcgca 1574

## RESULT 21

AAA81472/C  
ID AAA81472 standard; DNA; 16526 BP.

AAA81472;  
04-DEC-2000 (first entry)

N. meningitidis partial DNA sequence gnm\_20 SEQ ID NO:20.

Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;  
antigen; vaccine; diagnosis; infection; antibacterial; identification;  
Meningococcus B; MenB; ds.

Neisseria meningitidis.

W020002430-A2.

20-APR-2000.

08-OCT-1999; 99WO-US23573.

09-OCT-1998; 98US-0103794.

30-APR-1999; 99US-0132068.

(CHIR) CHIRON CORP.

Fraser CM, Hickey E, Peterson J, Tettelin H, Venter JC;  
Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scalato V;  
Rappuoli R, Piza M;

WPI: 2000-318079/27.

Isolated nucleotide sequences of Neisseria meningitidis which can be  
used in the diagnosis and treatment of N. meningitidis infection and  
other Neisserial infections, for example, N.gonorrhoea -

Claim 7: Page 466-471; 1760pp; English.

The present invention describes methods of obtaining immunogenic  
proteins from Neisseria genomic sequences. AAA81453 to AAA82414  
represent specifically claimed Neisseria meningitidis genomic DNA  
sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent  
Neisseria DNA sequences and their corresponding proteins; AAA81254 to  
AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the  
isolation of Neisseria meningitidis DNA sequences; and AAA81322 to  
AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF  
sequences, which are all used in the exemplification of the present  
invention. The nucleic acid sequences, protein sequences, and antibodies  
against them, can be used in the manufacture of a composition. The  
composition can be used as a medicament (or in the manufacture of a  
medicament) for treating, preventing or diagnosing infection due to  
Neisserial bacteria. For example, some of the identified proteins could

CC be components of vaccines against *Meningococcus B*; against all serotypes;  
 CC and/or against all pathogenic *Neisseriae*; identification of sequences  
 CC from the bacterium will also facilitate production of biological probes,  
 CC particularly organism-specific probes. Attempts to make efficacious  
 CC *Meningococcus B* vaccines have failed mainly due to antigen tolerance.  
 CC Multivalent vaccines have also been tried but none have successfully  
 CC overcome antigenic variability. The provision of further, complete  
 CC sequences may provide an opportunity to identify secreted or surface  
 CC exposed proteins that may be presumed targets for the immune system and  
 CC which are not antigenically variable or at least more conserved than  
 CC other more variable regions.

SO Sequence 16526 BP; 3183 A; 4006 C; 5067 G; 4268 T; 2 other:

Query Match 4.0%; Score 174.4; DB 21; Length 16526;  
 Best Local Similarity 60.5%; Pred. No. 8.2e-38;

Matches 305; Conservative 0; Mismatches 196; Indels 3; Gaps 1;

QY 1212 atgatactaccgaacatcaatcaatgctgtaggattatattccaaagagattt 1271  
 DB 7246 ACTGATGCTGGGACCAATATACCAAGGCGGCGCATTTGACAGCAACTT 7187  
 QY 1272 taggtctgcctgaaataaagaacttgcaagcgcggtcatalcagtgaga 1331  
 DB 7186 CACCGTC---GTGGTAAACCAACACATGCAAGTGCAGGCTTATCGTAGCCGACGG 7130  
 QY 1332 cagtaacgttactgaaagtaagcggtgcaaacgacgctggtccaaatcgagaa 1391  
 DB 7129 CAAACGCGTCTTGTGGAAGTACGACACCCAAAGGCGGCGCTTCCAAACTGGGCGC 7070  
 QY 1392 aggcagcgctgcagcttcaagcgaagggaaccgaagctcgatcgatggtgagcg 1451  
 DB 7069 AAGGCAAGCTTATCGCAACGAGCAAGGATCACCAGGCGGAGCATCGAGTGGGGAAG 7010  
 QY 1452 tacaactatttgatcgacgacgaagataaaggaataaataaacccttgatgaat 1511  
 DB 7009 CACTGTGCGACTCGCCCAAAAGCTCTTCAAGCGGACGCAAAACATTTCAACCAAGT 6950  
 QY 1512 cggcttgatcgagcggaaggatgacgtgcaactgaaatgacgataatgattcaaccgga 1571  
 DB 6949 CGGCATTCACAGCGGACGCGGCGGCTCTCGCCGACAGCGCAAAATCAACCCGA 6890  
 QY 1572 caaactcatttcgcttcgacgacgacgttgatttaagggcattcgcttcgtt 1631  
 DB 6889 AAACCTCATTTTGGCTTCAAGGGGAGGCGCTGACCTCAAGCGCAACCTTCCCTT 6830  
 QY 1632 ccacgatttcaaaataacgataagggcgatgattgtaaccacacatcaagacaaga 1691  
 DB 6829 TACCCATATTCGCGCATGCGGAGCGGCGCAATGCTCATACACACCTTACCAAGC 6770  
 QY 1692 atcacacgttaccattcaagga 1715  
 DB 6769 CGCGACACTGACGCTGACCGGCA 6746

RESULT 22  
 ID AAF21613 standard; DNA; 172325 BP.

XX AAF21613;  
 XX 13-MAR-2001 (first entry)

DE *Neisseria meningitidis B* nucleotide sequence SEQ ID NO:114.

KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; immunogenic; vaccine;  
 KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;  
 OS *Neisseria meningitidis*.

XX PN W0200066791-A1.

XX 09-NOV-2000.  
 PD 08-MAR-2000; 2000MO-US05928.  
 XX 30-APR-1999; 99US-0132068.  
 PR 08-OCT-1999; 99WO-US23573.  
 XX 28-FEB-2000; 2000GB-0004695.  
 PA (CHIR) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.

PI Pizze M, Hickey E, Peterson J, Tettelin H, Venter JC, Maignani V;  
 PI Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V, Rappuoli R;  
 PI Frazer CM, Grandi G;

WPI: 2000-647603/62.

Neisseria meningitidis B full length genome sequence and open reading  
 frames are used to detect, treat and prevent *Neisseria* infections -  
 Claim 7: Appendix A; 692pp: English.

The present invention describes the full length genome of  
*Neisseria meningitidis B* (NMB). The sequences in AAF21544 and AAF21607  
 to AAF21613 represent fragments of the NMB genomic sequence, as the  
 sequence was too long to go in a record on its own it was split into 8  
 sequences which overlap each other at the beginning and end of each  
 sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at  
 the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated at  
 the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the  
*Neisseria* proteins given in AAB58550 to AAB58593, and AAF21589 to  
 AAF21606 represent PCR primers which are used in the exemplification of  
 the present invention. The NMB genome and fragments from it have  
 antibacterial activity, and can be used in vaccines and gene therapy.  
*Neisseria* nucleic acids, proteins and/or antibodies which binds to the  
 proteins can be used in compositions for treating or preventing infection  
 due to *Neisseria* bacteria or as a diagnostic reagent for detecting the  
 bacteria. Computers, computer memory, computer storage medium or computer  
 databases can be used in a search to identify open reading frames (ORFs)  
 or coding sequences within the NMB genome. The DNA sequences provide  
 further opportunities to find antigenic or immunogenic proteins which are  
 more effective in vaccines than the outer membrane proteins currently  
 used.

Sequence 172325 BP; 43072 A; 47583 C; 41465 G; 40205 T; 0 other;

Query Match 4.0%; Score 174.4; DB 21; Length 172325;  
 Best Local Similarity 60.5%; Pred. No. 3.8e-38;

Matches 305; Conservative 0; Mismatches 196; Indels 3; Gaps 1;

QY 1212 atgatactaccgaacatcaatcaatgctgtaggattatattccaaagagattt 1271  
 DB 8192 actgatctgtgcagacacatacaacgaagcgagcgatgctgtaggacgaactt 8251  
 QY 1272 taggtctgcctgaaataaagaacttgcaagcgcggtcatalcagtgaga 1331  
 DB 8252 caccgctc---gtcgtaaaacacacacatgcaagtgcaagcgtatgtagcgacg 8308  
 QY 1332 cagtaacgttactgaaagtaagcggtgcaaacgacgctggtccaaatcgagaa 1391  
 DB 8309 caaagcgcttcttgcaagtcagcaaccccaagcgacgctctccaaacttgagcgc 8368  
 QY 1392 aggcagcgctgcagcttcaagcgaagggaacaaagctcgatcagcggtgagcgcg 1451  
 DB 8369 aggcagcgcttcaagcgaagcgaagcgaagcgaagcgaagcgaagcgaagcgaag 8428  
 QY 1452 tacaactatttgatcgacgacgacgacgacgacgacgacgacgacgacgacgacg 1511  
 DB 8429 cactgtcgtactcgcccaaaagctgcttcagcagcgacgacgacgacgacgacgacg 8488



FT RBS 248..253  
 FT //tag= d  
 PN MO9011367-A.  
 XX  
 PD 04-OCT-1990.  
 XX  
 PF 16-MAR-1990; 90WO-DK00073.  
 XX  
 PR 17-MAR-1989; 89DK-0001308.  
 XX  
 PA (KILL/) KILLIAN M.  
 XX  
 PI Killian M, Poulsen K;  
 XX  
 DR WPI: 1990-320267/42.  
 DR P-PSDB: AAR07304.  
 XX  
 PT Immunoglobulin A1 protease prodn. - by cloning from  
 PT microorganisms for immunisation against immunoglobulin A1  
 PT protease producing bacteria  
 XX  
 PS Disclosure; fig 3; 44pp; English.  
 XX  
 CC This iqa gene is from H.influenzae serotype b strain HK368. On  
 CC transformation of E.coli cells with a vector contg. this gene,  
 CC immunoglobulin (Ig)A1 protease is produced which is useful in a  
 CC vaccine for e.g. meningococcal meningitis, gonorrhoea or allergic  
 CC diseases.  
 XX  
 SQ Sequence 5091 BP; 1862 A; 873 C; 979 G; 1377 T; 0 other;

Query Match 3.4%; Score 149; DB 11; Length 5091;  
 Best Local Similarity 57.6%; Pred. No. 8,7e-32;  
 Matches 307; Conservative 0; Mismatches 220; Indels 6; Gaps 2;

QY 1198 gaagaaagcgaattgatacttaacagacaatcaatcaaggctgagagattat 1257  
 DB 1420 gaaggaagtggaaagcttaacttaataataatcatgaagctgagagattatc 1479  
 QY 1258 ttcaagaagattttagcgt---ctgcctgaataataagaacttggcagcgaggc 1314  
 DB 1480 ttgaagcgatttgaagtaagtaagtaactctgataactcttggaaagagagc 1539  
 QY 1315 gtcaatcagtgagaagcagtaactgtacttggaaagtaaacgctggcaacagcgc 1374  
 DB 1540 gtctctgtgcggaagaaactgtgaagctggaagtgataatcctcaatattgctg 1599  
 QY 1375 ctgtccaaatcgcaaaagcagctgcacgttcaagcacaagggggaaacacagctgc 1434  
 DB 1600 ttgaagaataatggcaaaagacatattatgttgaagagacagagataataagctgc 1659  
 QY 1435 atcagcgtggcgagcagctatcagcttggatcagcagcagcagcagataaagcaaaaa 1494  
 DB 1660 cttaagtggtgcagtgacacgttattttaaaacaacaacaatggttcggg---acaa 1716  
 QY 1495 caagcctttagtgaatcggttggcagcgagcgaggtgacggttcaactgagtcgcat 1554  
 DB 1717 cagcgttctgtctgttaggagattgtaagtggtgcgaacccctgtgttaatgagat 1776  
 QY 1555 aatcagttcaaccgcgaacaactcttccgcttgcgcggcgagcgttggatttaaac 1614  
 DB 1777 aaacaagtgatccaatccaatttaacttgcctttagggcggtgcgattagacttaaac 1836  
 QY 1615 gggcagcttgccttgcctcacgcttatacaaaatacagatgaagggcgatattgtaac 1674  
 DB 1837 ggaattcactaaccttgcatacacaatcagaatattgtatgagtgagcgaactgtaac 1896  
 QY 1675 caacaatcaagaagaatccacgcttaccattacagcaataaagatattgc 1727  
 DB 1897 cataatattgtaattgctccaataataacagattactctgggaagcctaattac 1949

RESULT 25  
 ID ABA89172  
 XX ABA89172 standard; DNA; 4113 BP.  
 AC ABA89172;  
 XX  
 DT 11-FEB-2002 (first entry)  
 XX  
 DE Escherichia coli polynucleotide SEQ ID NO 890.  
 XX  
 KW Escherichia coli; B2/D-A; antiinflammatory; antibacterial;  
 KW immunosuppressive; extra-intestinal infection; phylogeny; meningitis;  
 KW systemic infection; non-diarrhoeal infection; septicaemia;  
 KW pyelonephritis; antibiotic resistance; ds.  
 XX  
 OS Escherichia coli.  
 XX  
 PN WO20016572-A2.  
 XX  
 PD 13-SEP-2001.  
 XX  
 PE 12-MAR-2001; 2001WO-EP03445.  
 XX  
 PR 10-MAR-2000; 2000FR-0003145.  
 PR 02-FEB-2001; 2001FR-0001449.  
 XX  
 PA (INRM ) INSERM NAT SANTE & RECH MEDICALE.  
 XX  
 PI Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;  
 XX  
 DR WPI: 2001-550253/61.  
 XX  
 PT A library of DNA fragments of Escherichia coli strains for the  
 PT phylogenetic determination of a given strain comprises polynucleotides of  
 PT nature B2/D+ A - -  
 XX  
 PS Example 6; fig 6; 646pp; English.  
 XX  
 CC The invention relates to a library of DNA fragments of Escherichia coli  
 CC strains comprising polynucleotides (ABA88577-ABA88872 and ABA89533)  
 CC and encoded proteins (AB852459-AB852919 and AB852954-AB853094) of nature  
 CC B2/D+A-. The polynucleotides have potential antiinflammatory,  
 CC antibacterial and immunosuppressive activity as part of pharmaceutical  
 CC compositions used to treat, palliate or prevent extra-intestinal E. coli  
 CC infections. The polypeptides are useful for determining the phylogenetic  
 CC group of a given E. coli strain. These polypeptides can detect and treat  
 CC an undesired development of E. coli, particularly an extra-intestinal  
 CC infection that include systemic and non-diarrhoeal infections such as  
 CC septicaemia, pyelonephritis and meningitis this is particularly  
 CC advantageous as bacterial resistance is increasing with the more  
 CC frequent use of broad spectrum antibiotics.  
 XX  
 SQ Sequence 4113 BP; 1112 A; 950 C; 1105 G; 946 T; 0 other;

Query Match 3.1%; Score 135; DB 22; Length 4113;  
 Best Local Similarity 53.8%; Pred. No. 8.6e-28;  
 Matches 279; Conservative 0; Mismatches 240; Indels 0; Gaps 0;

QY 1171 aatgagaataatttccttattgacgagaagaagcgattgatacttaacagcaac 1230  
 DB 1051 aatgcggtataaataatctgtattcagcgagcagagcgtgacattgtcttgaagacagt 1110  
 QY 1231 atcaatcaaggtgctgagattatattccaagagaattttagcgttcgctgaaat 1290  
 DB 1111 gtgactcagggggcggtatcctgaatttaagcaggttacacgctatcgtcgatcc 1170  
 QY 1291 aacgaacttggcagagcgcggttcatatcagtgagcagctacacgttaactggaag 1350  
 DB 1171 ggaataaacttgagcggtgagcatttacttgaacaagggaggaatgtgacctggaag 1230  
 QY 1351 gtaacggtggtgcaaacgacgcctgtccaaatcggaagcagcgttcgacgttcaa 1410

DB 1231 gtcaacggggttgcggtgacacccgataaattggggaaggaacccgaccataaac 1290  
OY 1411 gccaaagggaacaaacagctcagtcagcgttggcgacggtacatcatttggatcag 1470  
DB 1291 ggaacaggtgttaaacccggggagactgaaacgggagacggtacccgttgaactaacag 1350  
OY 1471 cagcagacgataaaggcaaaaacacgctttagtgaatcgttggcagcggcagg 1530  
DB 1351 cagcagacgatacgcaggttaattgttcagccttcagttccgtaaccgcgcagcgaga 1410  
OY 1531 ggtacgttcacactgaatgcagataatcagttcaaccgcgaacacatctatttcgctt 1590  
DB 1411 ccgacccgtgtgtctcgggagatgcccgtcaggtcaatccggatacatttcaatgggagac 1470  
OY 1591 cgcgcgcagcgttggattaaacgggcatcgcgttccgtccacggtatcaataacc 1650  
DB 1471 cggggaggttaagcttgcaccttaattgttaattgcgttacccttcacccgactgcaggtcgc 1530  
OY 1651 gatgaaggggcgatgattgttcaaccacaatcaagacaaa 1689  
DB 1531 gattacggggcggtgattacataataatgcacagcaaaa 1569

## RESULT 26

ABA89141/C

ID ABA89141 standard; DNA; 48254 BP.

AC ABA89141:

DT 11-FEB-2002 (first entry)

XX Escherichia coli polynucleotide seq ID NO 829.

DE Escherichia coli polynucleotide seq ID NO 829.

KW Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;

KM immunosuppressive; extra-intestinal infection; phyllosy; meningitis;

KW systemic infection; non-diarrhoeal infection; septicaemia;

KM pyelonephritis; antibiotic resistance; ds.

OS Escherichia coli.

PN WO200166572-A2.

PD 13-SEP-2001.

XX 12-MAR-2001; 2001MO-EP03445.

PE 10-MAR-2000; 2000PR-0003145.

PR 02-FEB-2001; 2001FR-0001449.

XX (INRM ) INSERM INST NAT SANTE &amp; RECH MEDICALE.

PA Blngen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;

PI WPI: 2001-550253/61.

XX Example 6; Fig 6; 646pp; English.

XX The invention relates to a library of DNA fragments of Escherichia coli  
CC strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533)  
CC and encoded proteins (AB852459-AB852919 and AB852954-AB853094) of nature  
CC B2/D+A-. The polynucleotides have potential antiinflammatory,  
CC antibacterial and immunosuppressive activity as part of pharmaceutical  
CC compositions used to treat, palliate or prevent extra-intestinal E. coli  
CC infections. The polypeptides are useful for determining the phylogenetic  
CC group of a given E. coli strain. These polypeptides can detect and treat  
CC an undesired development of E. coli, particularly an extra-intestinal  
CC infection that include systemic and non-diarrhoeal infections such as  
CC septicaemia, pyelonephritis and meningitis this is particularly

CC advantageous as bacterial resistance is increasing with the more  
CC frequent use of broad spectrum antibiotics.  
XX Sequence 48254 BP; 12342 A; 11284 C; 12417 G; 12211 T; 0 other;

Query Match 3.18; Score 135; DB 22; Length 48254;  
Best Local Similarity 53.88; Pred. No. 4.3e-27;  
Matches 279; Conservative 0; Mismatches 240; Indels 0; Gaps 0;

OY 1171 aatggagaataatttcccttattgacgaagaaagcgaaattgacttaccagcaac 1230  
DB 28948 AATGCCGCTAAATATCTGTGTTTACGCGGGGACAGCGTCAATTCGCTGAAGACACT 28889  
OY 1231 atcaatcaaggtgtcgtgagatatttccaaaggaattttagtctgcctggaat 1290  
DB 28888 GTGACTTACGGGGCGCGCTTATCTCGAATTAAACAGTTACACCGTATCTGTGATCC 28829  
OY 1291 aacgaacttggcaaggcgcggttcataatcagtgaaagacgtacgttacttgaaa 1350  
DB 28828 GGAAAAACCTGGACGGGTGCGGCTTATTTACTGACAAAGGAGCGATGTGACCTGGAAG 28769  
OY 1351 gtaacgcggttgcgaacagcgcctgtccaaatcggcaaaagcgacgtcagctcaa 1410  
DB 28768 GTCAACGGGGTTCGCCGGTACACCTGCATTAATTGGGGGAGAGACCTGACCATTAAC 28709  
OY 1411 gccaaagggaacaccaggtcgtcagtcagcgttggcgaggttaccatttggatcag 1470  
DB 28708 GGAAACAGGTGTAAACCCGGGAGACTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 28649  
OY 1471 cagcagcagcagataaaggcaaaaacacgctttagtgaatcgttggcagcggcagg 1530  
DB 28648 CAGGACAGACTGTCAGATTAATTTCAGGCTTTCGTAACCTTCGTAACCTTCGTAACCT 28589  
OY 1531 gttacgttcacactgaatgataatcagttcaaccgcgaacacatctatttcgctt 1590  
DB 28588 CCGACCGTGTCTCGGAGATCCCGTCAGGTCATTCGGAATTCATTCATTCATTCATTC 28529  
OY 1591 cgcgcgcagcgttggattaaacgggcatcgcgttccgtccacggtatcaataacc 1650  
DB 28528 CCGGAGAGGTAACTGATTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAAT 28469  
OY 1651 gatgaaggcgatgattgttcaaccacaatcaagacaaa 1689  
DB 28468 GATTACGGGGCGGTGATTACAAATATATGACAGCAAAAA 28430

## RESULT 27

ABA89142/C

ID ABA89142 standard; DNA; 48345 BP.

AC ABA89142:

DT 11-FEB-2002 (first entry)

XX Escherichia coli polynucleotide seq ID NO 830.

DE Escherichia coli polynucleotide seq ID NO 830.

KW Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;

KM immunosuppressive; extra-intestinal infection; phyllosy; meningitis;

KW systemic infection; non-diarrhoeal infection; septicaemia;

KM pyelonephritis; antibiotic resistance; ds.

OS Escherichia coli.

PN WO200166572-A2.

PD 13-SEP-2001.

XX 12-MAR-2001; 2001MO-EP03445.

PE 10-MAR-2000; 2000PR-0003145.

PR 02-FEB-2001; 2001FR-0001449.

XX

PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 XX Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C,  
 XX WPI; 2001-550253/61.  
 XX

PT A library of DNA fragments of *Escherichia coli* strains for the  
 PT phylogenetic determination of a given strain comprises polynucleotides of  
 PT nature B2/D+ A-.

PS Example 6; Fig 6; 646bp; English.

CC The invention relates to a library of DNA fragments of *Escherichia coli*  
 CC strains comprising polynucleotides (AB88577-AB88729 and AB88533)  
 CC and encoded proteins (AB852459-AB852919 and AB852954-AB853094) of nature  
 CC B2/D+A-. The polynucleotides have potential anti-inflammatory,  
 CC antibacterial and immunosuppressive activity as part of pharmaceutical  
 CC compositions used to treat, palliate or prevent extra-intestinal *E. coli*  
 CC infections. The polypeptides are useful for determining the phylogenetic  
 CC group of a given *E. coli* strain. These polypeptides can detect and treat  
 CC an undesired development of *E. coli*, particularly an extra-intestinal  
 CC infection that include systemic and non-diarrhoeal infections such as  
 CC septicæmia, pyelonephritis and meningitis this is particularly  
 CC advantageous as bacterial resistance is increasing with the more  
 CC frequent use of broad spectrum antibiotics.

CC Sequence 48345 BP; 12347 A; 11290 C; 12423 G; 12219 T; 66 other;

Query Match 3.1%; Score 135; DB 22; Length 48345;  
 Best Local Similarity 53.8%; Pred. No. 4.3e-27;  
 Matches 279; Conservative 0; Mismatches 240; Indels 0; Gaps 0;

QY 1171 aatggaataatattcttattgacgaagaaagcgatgactaccagaac 1230  
 DB 28948 AATGCCGTAATAATCTGTGTTTCAGCGGAGAACCGCAATTTGCTGGAAGACAGT 28889  
 QY 1231 atcaatcaagtgtctggaagattatccaaagagatttaccgctgcctgaat 1290  
 DB 28888 GTGACTCAGGGGGCGGTTATCTCGAATTGTAAGACAGTACACCGTATCGTGAATCC 28829  
 QY 1291 aacgaacttgcaagcgcggttcacatacgtgaagaacgcttacttgga 1350  
 DB 28828 GGAAAAACCTGAGCGGCGCGGCAATTATTAAGCAAGGGGAGCATGTGACCTGGAG 28769  
 QY 1351 gtaaacggtgtgcaaacgacgcgttccaaatcgcaagcgacgcgtgcgttcaa 1410  
 DB 28768 GTCAACGGGTTGCCCGGTGACAACTGCAATAATTGGGGAGAGAACCCGACCAATAAC 28709  
 QY 1411 gccaaaggggaaacaaagctcgtatgacgttggtgacggtacagcttggatcag 1470  
 DB 28708 GGAAACGTTGTAACCCGGGAGGACTGAATAACGGGAGACGTCGCTTGACTTAACAG 28649  
 QY 1471 caagcagcagataaagcaaaacaaagccttgaagaaatcggttgcgcgcagcag 1530  
 DB 28648 CAGCAGACACTGACAGTAAATGTTACAGGCTTCAGTTCCGTGAACCTCCGACGAGCA 28589  
 QY 1531 gttacggtgcaactgaatgcgataatcagattcaacccgcgaacaaacttattcgctt 1590  
 DB 28588 CCGACCTGCTGCTCGAGATGCCCGGACAGTCAATCCGATTAACATTTCATGGGATAC 28529  
 QY 1591 cggcgcggaactgtgataaagcgatcgttgcgttccacacgataataatcc 1650  
 DB 28528 CGGGAGGATTAAGCTTGACCTTAATGTAATGCCGTTACCTTCAACCCGACCTGACGCTGCC 28469  
 QY 1651 gatgaagggcgatgattgtcaacacaatcaagacaa 1689  
 DB 28468 GATTACGGGGGCTGATTCAAAATATGCAACAGCAAAAA 28430

RESULT 28  
 ABA88994  
 ID ABA88994 standard; DNA; 4128 BP.

XX ABA88994;  
 AC  
 XX  
 XX 11-FEB-2002 (first entry)  
 DT  
 XX

DE *Escherichia coli* polynucleotide SEQ ID NO 559.

XX *Escherichia coli*; B2/D+A-; anti-inflammatory; antibacterial;  
 KW immunosuppressive; extra-intestinal infection; phylogeny; meningitis;  
 KW systemic infection; non-diarrhoeal infection; septicæmia;  
 KW pyelonephritis; antibiotic resistance; ds.

OS *Escherichia coli*.

PN WO200166572-A2.

PD 13-SEP-2001.

PF 12-MAR-2001; 2001WO-EP03445.

PR 10-MAR-2000; 2000FR-0003145.

PR 02-FEB-2001; 2001FR-0001449.

XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PI Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;

DR WPI; 2001-550253/61.

PT A library of DNA fragments of *Escherichia coli* strains for the  
 PT phylogenetic determination of a given strain comprises polynucleotides of  
 PT nature B2/D+ A-.

XX Example 6; Fig 6; 646bp; English.

CC The invention relates to a library of DNA fragments of *Escherichia coli*  
 CC strains comprising polynucleotides (AB88577-AB88729 and AB88533)  
 CC and encoded proteins (AB852459-AB852919 and AB852954-AB853094) of nature  
 CC B2/D+A-. The polynucleotides have potential anti-inflammatory,  
 CC antibacterial and immunosuppressive activity as part of pharmaceutical  
 CC compositions used to treat, palliate or prevent extra-intestinal *E. coli*  
 CC infections. The polypeptides are useful for determining the phylogenetic  
 CC group of a given *E. coli* strain. These polypeptides can detect and treat  
 CC an undesired development of *E. coli*, particularly an extra-intestinal  
 CC infection that include systemic and non-diarrhoeal infections such as  
 CC septicæmia, pyelonephritis and meningitis this is particularly  
 CC advantageous as bacterial resistance is increasing with the more  
 CC frequent use of broad spectrum antibiotics.

CC Sequence 4128 BP; 1151 A; 945 C; 1052 G; 980 T; 0 other;

Query Match 2.7%; Score 118.4; DB 22; Length 4128;  
 Best Local Similarity 53.7%; Pred. No. 5.6e-23;  
 Matches 245; Conservative 0; Mismatches 211; Indels 0; Gaps 0;

QY 1232 tcaatcaaggtgtctggaaggttatattccaaaggaatttaccgctgcgcgtaata 1291  
 DB 1115 tcaagcgaggtgtcgcgttaccatctgatactgatactacacgttccacattcaaacg 1174  
 QY 1292 acgaacttggcaagcgcggttcacatacagltgaagaacagcttacttggaag 1351  
 DB 1175 gaagtaacttgacccggcggttattgttggaagaagatgcccgcgtaaacgtggcag 1234  
 QY 1352 taagaagcggtgcaaacgcgcgttccaaatcgcaagcgacgttcaggttcaag 1411  
 DB 1235 ttaatgtgtgaaagggtgacaaccttcaataatcggaagaacccgtgttgtaacg 1294  
 QY 1412 ccaaaaggggaaacaaagcgtcatcagcgttggcgacgtacagtttggatcagc 1471  
 DB 1295 gaaccggtgttaatggcgcgccgtgaagatcggggaatgggaacgttgcctcaatcagc 1354  
 QY 1472 aggcagacagataaaggcaaaacaaagccttgaatcggttgcgcgcagcag 1531



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||||| 111 1 111 1 111 11111111
Db 1355 agcgagacagttcagacagttcagatcagtagcgtgaatattgcccagcgccg 1414
Qy 1532 gtaagcgtcaactatgacgataatcagttcacccgcaactatattcggttc 1591
Db 1415 cgagcgtcgtgtgacagacacacgaggttaacccgaataatattcctgggtacc 1474
Qy 1592 gcgcgcagcgtttgattaaacgggcatctgccttcgtccacggtatcaaatccg 1651
Db 1475 gggggggggttctggtatgttaacggaatgacgtgaattcattgaagctgaatgcgcg 1534
Qy 1652 atgaagggcgatgattgtcaaccacatcaagca 1687
Db 1535 attatgcgcaactctcgttaacagcagtgataa 1570

RESULT 29
ABA88991/c
ID ABA88991 standard: DNA: 7654 BP.
XX
AC ABA88991;
XX
Dt 11-FEB-2002 (first entry)
XX
DE Escherichia coli polynucleotide SEQ ID NO 554.
XX
KW Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;
KW immunosuppressive; extra-intestinal infection; phylogeny; meningitis;
KW systemic infection; non-diarrhoeal infection; septicemia;
KW pyelonephritis; antibiotic resistance; ds.
XX
OS Escherichia coli.
XX
PN WO200166572-A2.
XX
PD 13-SEP-2001.
XX
PF 12-MAR-2001; 2001MO-EP03445.
XX
PR 10-MAR-2000; 2000FR-0003145.
XX
PR 02-FEB-2001; 2001FR-0001449.
XX
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;
XX
DR WPI: 2001-550253/61.
XX
PT A library of DNA fragments of Escherichia coli strains for the
PT phylogenetic determination of a given strain comprises polynucleotides of
PT nature B2/D+ A- -
XX
PS Example 6; Fig 6; 646pp; English.
XX
XX The invention relates to a library of DNA fragments of Escherichia coli
XX strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533)
XX and encoded proteins (ABBS2459-ABBS2919 and ABBS2954-ABBS3094) of nature
XX B2/D+A-. The polynucleotides have potential antiinflammatory,
XX antibacterial and immunosuppressive activity as part of pharmaceutical
XX compositions used to treat, palliate or prevent extra-intestinal E. coli
XX infections. The polypeptides are useful for determining the phylogenic
XX group of a given E. coli strain. These polypeptides can detect and treat
XX an undesired development of E. coli, particularly an extra-intestinal
XX infection that include systemic and non-diarrhoeal infections such as
XX septicaemia, pyelonephritis and meningitis this is particularly
XX advantageous as bacterial resistance is increasing with the more
XX frequent use of broad spectrum antibiotics.
XX
SQ Sequence 7654 BP; 2000 A; 1697 C; 1656 G; 2301 T; 0 other;

```

Query Match 2.7%; SCORE 118.4; DB 22; Length 7654;  
 Best Local Similarity 53.7%; Pred. No. 8.4e-23;

```

Matches 245; Conservative 0; Mismatches 211; Indels 0; Gaps 0;
Qy 1232 tcaatcaagtgctgagggattatattccaaggaattttaggtctgcctgaaata 1291
Db 4592 TCACGCAAGGTCGGGTTCACTGACATTTCGTGTGACTACATGTCACACTTCAAAAG 4533
Qy 1292 acgaacttgcaaggcgcggttcaatacagtgaaagacagtaacgttaactggaag 1351
Db 4532 GAAGTACTGTGACCGGGGCGGTATTTATGTGCAAGATGCTCCGTAACTGTGCAGG 4473
Qy 1352 taacgcgttgcaaaagcgcctgtccaaataatcggaagacagcgttcagttcaag 1411
Db 4472 TTAATGTGTGAAGGTGACCACTGCATTAATAATGGCGAAGAACCTTGTTGTACAG 4413
Qy 1412 ccaaaagggaaaacccaagcgtcagtcagcgtggtgagcaggttaacgttaattggtacagc 1471
Db 4412 GAACCGGTGTTATAGAGGCGGCGCTGAAGAATCGGGGATGGAGCGTGTGCTCAATCAG 4353
Qy 1472 agcgacagataaaggcaaaaaaagaagcctttagtaacgtcgttgcagcgagga 1531
Db 4352 AGCGTGACAGTTCAAGGACACGCTCAGGCATTCACTAGCGTGAATATTGCCAGGCGCCG 4293
Qy 1532 gtaaggtgaactgaatgcgataatcagttcaaacccgacaactatattcggttc 1591
Db 4292 CGACGTCTGCTGCGCAACACACAGCAAGTTAATCCGACATATATCCGTGGGCTACG 4233
Qy 1592 gcgcgcagcgtttgattaaacgggcatctgccttcgttcacggtatcaaatccg 1651
Db 4232 GGGGGGGGTTCTGTGATGTTAAGCGGAATGACCTGACATTTTCATTAAGCTGAATCCGCCG 4173
Qy 1652 atgaagggcgatgattgtcaaccacatcaagca 1687
Db 4172 ATTTATGCGCAACTCTGTTGATACAGCAGTGAATAA 4137

RESULT 30
AAA81786/c
ID AAA81786 standard: DNA: 116 BP.
XX
AC AAA81786;
XX
Dt 04-DEC-2000 (first entry)
XX
DE N. meningitidis partial DNA sequence gnm_333 SPO ID NO:333.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW Meningococcus B; MenB; ds.
XX
OS Neisseria meningitidis.
XX
PN WO200022430-A2.
XX
PD 20-APR-2000.
XX
PF 08-OCT-1999; 99MO-US23573.
XX
PR 09-OCT-1998; 98US-0103194.
XX
PR 30-APR-1999; 99US-0132068.
XX
PA (CHIR ) CHIRON CORP.
XX
PI Frazer CM, Hickey E, Peterson J, Rettelin H, Venter JC;
PI Masiangian V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappunoli R, Pizsa M;
XX
WPI: 2000-318079/27.
XX
PT Isolated nucleotide sequences of Neisseria meningitidis which can be
PT used in the diagnosis and treatment of N. meningitidis infection and
PT other Neisserial infections, for example, N.gonorrhoea -
XX
PS Claim 7; Page 1597; 1760pp; English.

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50 Sequence 1859 BP; 316 A; 617 C; 619 G; 307 T; 0 other;

**Qy**    3213 agccaaaaacagcgcggaataaacacgcaagaaccttgcgcgcgtgatlycggccg    3277  
       |||    |||    |||    |||    |||    |||    |||    |||    |||    |||  
**Db**    769 AGCTCAGCCACGGCAGGAAGTCGACACCTTTGAAGCGCGCAACAAGCTTCGAGAACCTCT    710

59 AGCTCAGCCACGGCAGGAGTCCGACGACGTTGAAGGGCGCCGAACAGCTTCGAGA 710

709 GCAGATGGCGATCACTCCTCTGTGTCCTGCGCGGTGCGCAAGGCGCGGGA 650

QY 3333 aaacgctcgcatactgcagcgcgaggaagagaaaaaacggtctgcagcgcgataaagacac 3392

QY 3393 cgcttgcgaacagcgcgaagcggaaaccgcgcgcgtaccacgccttccccgcgc 3452

OY		CGCCGAGGGGCCACCTCCTGCACAGGCCACC	530
Dβ	589	CGCCGCCCCGGCACCGCCCCTTCGCGACGGGCCACC	630
3453	CGCCGAGGGGCCACCTCCTGCACAGGCCACC		

Db  
529 ACGTCCTCGGGCGGGCGCCGGCTGACACACTTCATCATCAGCACAGCTTGGCGATCTGGCGCC 470

Db	469	AGA	467
----	-----	-----	-----

## RESULT 34

ID	AA199663	standard; DNA; 4403765 BP.
ID	AA199663	
XX	AA199663	

15-JAN-2002 (first entry)

Mycobacterium tuberculosis: strain H37Rv. genome SEQ ID NO 2.

variation; epidemiology; patient treatment; epidemic monitoring; ds.  
Mycobacterium tuberculosis.

US6294328-B1.

24-JUN-1998; 98US-0103840.

PR 24-JUN-1998; 98US-0103840.  
XX  
(GENO-) INST GENOMTC PPS  
PA

Frerschmann RD, White OR, Fraser CM, Venter JC  
WPI: 2001-647261/74.

determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where *M. tuberculosis* strains CDC 1551 and H37Rv differ -

PS Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English  
XX

The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, *Mycobacterium tuberculosis* or related *Mycobacterium* by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of *M. tuberculosis* strains CDC 1551 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of *M. tuberculosis* and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic monitoring.

CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from USPO  
CC at [seqdata.uspto.gov/sequence.html?DocID=62993288B1](http://seqdata.uspto.gov/sequence.html?DocID=62993288B1).  
CX

Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;

Query Match	1.0%	Score 45.4	DB 22	Length 4403765
Best Local Similarity	51.6%	Pred. No. 7.4		
Matches 127	Conservative	0	Mismatches 119	Indels 0
			Gaps	0

[illegible]

QY 3791 acgacggcatcgcgcaactcgcgcacgcgttcgccacgcgcgccgttttcgcgcataatcgcga 3850

OY 3851 tcgacaggttctacatcgcatcaggccggcgqgcgqqltttaagcaagcgaacctttaa 3910  
DD 2422030 ggaaagtcggcagcggccccccacggcggttaaaagcgcagcgttgtaacggsgccaacggcg 2422031

Db 2422030 GCACGCGCGTGTGATCGGCAACGGCGCGCGCGCGCTTCGGCATACCG 2421971

Db 2421970 TCGGAAGTGGTGGTGCCTGGTGTCTTTCGGACACCCCTGGAGCAACG 2421911

b2421910 ggcggc 2421905  
|||  
qy 3971 ggcgcg 3976

## RESULT 35

ABL140/4  
ID ABL14674 standard; cDNA; 4461 BP.  
XX

26-MAR-2002 (first entry)

Drosophila melanogaster expressed polynucleotide SEQ ID NO 38504.

**pharmaceutical; gene; ss.**

XX  
XX  
PN  
XX  
W0200171042-A2.  
XX

ED  
4/-SEP-2001.  
XX

PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI: 2001-656860/75.  
 DR P-PSDB: ABB70571.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from *Drosophila* and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Claim 1: SEQ ID NO 38504; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA  
 CC sequences (AB101840-AB116175) and the encoded proteins.  
 CC (AB57737-AB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SQ Sequence 4461 BP; 1272 A; 1117 C; 960 G; 1112 T; 0 other;  
 Query Match 1.0%; Score 45.2; DB 23; Length 4461;  
 Best Local Similarity 51.5%; Pred. No. 0.095; Indels 0; Gaps 0;  
 Matches 104; Conservative 0; Mismatches 98;  
 QY 3735 cggcagcggcgccgctcgttcttcgcacacgcgacgaaacacgttcagca 3794  
 DB 589 cgtcatggaagtcggtcgccaccgctggcagcgcgacccgcagcagcaagaacatgg 648  
 QY 3795 cggcagcgaactcggcagcgttcgccacggcgccgttttcgggcaatacgcacga 3854  
 DB 649 cggcggcagcagcagcagcagcgggtggcgccgttgcaacatcgaactcgttcggcgc 708  
 QY 3855 caggtttacatcggcagcagcggcggttttagcagcggcagcagcgttcagca 3914  
 DB 709 cagcggcagcagcagcagcagcggcgccagtttccagcaagaacagcgttcgca 768  
 QY 3915 catcgagcgaataatccgcgc 3936  
 DB 769 cagcagcagcgaacacgcagcagc 790  
 RESULT 36  
 AAA70218  
 ID AAA70218 standard; DNA: 1212 BP.  
 XX  
 AC AAA70218;  
 XX  
 DT 07-NOV-2000 (first entry)  
 XX  
 DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:351.  
 XX  
 KW Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine;  
 KW antimalarial; malaria; protozoa; infection; insecticide; ds.  
 XX  
 OS Plasmodium falciparum.  
 XX  
 WO200025728-A2.  
 XX  
 PD 11-MAY-2000.  
 XX

PF 05-NOV-1999; 99WO-US26796.  
 XX  
 PR 05-NOV-1998; 98US-0107131.  
 XX  
 PA (HOFF/) HOFFMAN S.  
 PA (CARU/) CARUCCI D.  
 PA (GARD/) GARDNER M.  
 PA (VENT/) VENTER J C.  
 XX  
 PI Hoffman S, Carucci D, Gardner M, Venter JC;  
 XX  
 DR WPI: 2000-365347/31.  
 XX  
 PT Proteins encoded by chromosome 2 of the human malarial parasite,  
 PT Plasmodium falciparum, useful as antimalarial vaccines and in the  
 PT diagnosis of *P.falciparum* infection -  
 XX  
 PS Disclosure; Page 541; 577pp; English.  
 XX  
 CC The present invention describes proteins and their fragments (I) encoded  
 CC by chromosome 2 of the human malarial parasite, *Plasmodium falciparum*.  
 CC Also described are: (1) nucleotide sequences (II) encoding (I); and (2)  
 CC vaccines against *P. falciparum* infection comprising (I) or (II).  
 CC (I) and (II) are useful for the development of vaccines against  
 CC *P. falciparum* infection. (1) and polyclonal antisera or a monoclonal  
 CC antibody raised to immunogens comprising the sequences of (I) are  
 CC useful in the detection of infection with *P. falciparum*. Furthermore,  
 CC (I) (especially when they are rifins or secreted or membrane proteins)  
 CC can aid the identification of drugs to treat or prevent *P. falciparum*  
 CC infection, or they can be used to identify drug resistance in  
 CC *P. falciparum*. Sequencing of the *Plasmodium* chromosome 2 and the  
 CC subsequent identification of proteins encoded by it will help to expand  
 CC our understanding of parasite biology, a process hampered by the  
 CC complexity of the parasitic lifecycle, and provide new targets for  
 CC vaccine and drug development. Parasite resistance to drugs and mosquito  
 CC resistance to insecticides have led to a resurgence of malaria in many  
 CC parts of the world, and there is a pressing need for vaccines and new  
 CC drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide  
 CC and protein sequences given in the present invention, but which are not  
 CC specifically mentioned within the specification.  
 XX  
 SQ Sequence 1212 BP; 593 A; 113 C; 139 G; 367 T; 0 other;  
 Query Match 1.0%; Score 44.4; DB 21; Length 1212;  
 Best Local Similarity 48.1%; Pred. No. 0.069; Indels 0; Gaps 0;  
 Matches 126; Conservative 0; Mismatches 136;  
 QY 379 gaaggaagaatccgcagcaacatcgtttactataaattgtgaacggaataat 438  
 DB 112 gaagtaataataatgataaactataaataaattgccaacataagaataatgataatct 171  
 QY 439 aaagcaggactaaagccatccttatgctggcgagatcatatccggtttgataaa 498  
 DB 172 aatcaaatgycgaagataatacaaatgycgaagataatcaaatgycgaatcttaata 231  
 QY 499 ttgttcagatgcagaacctgttgaatgaccagatcatatgatgagcgaataatc 558  
 DB 232 aatgacgaacataaataatgataacataaataaataatgataacataatcaaatgac 291  
 QY 559 gatcaataatccttcagcgtgttcgattggggcagcagcgaataatggcgatc 618  
 DB 292 gaacataataatgacgaacataatcaaatgacgaacataatcaaatgataacat 351  
 QY 619 gatgaagatgagcccaataac 640  
 DB 352 aatcaaatgacgaacataatc 373  
 RESULT 37  
 AAA61800  
 ID AAA61800 standard; cDNA: 1231 BP.  
 XX

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Query Match      1.0%: Score 44; DB 21; Length 1231;
Best Local Similarity 43.2%: Pred. No. 0.091;
Matches 261; Conservative 0; Mismatches 340; Indels 3; Gaps 1

QY 3516 cctgacacgaccttaagcccaatagcgttttagtgaatatttcgcgcacgctcaacagcgt 3575
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 51 ccaacacgacactycaacgcacatgatgtgagactgcgcgtcagcagcagactgcgcctcgt 110

QY 3576 ttctgcgcacgaagcgaattagaccgcgtattttcgcgaacccgcgcgaagcgtttg 3635
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 111 cgcgcgcgcacgaagcgcgcgtcgtctcgtccgcgcgcgcgagcttgctcaagaatcca 170

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[illegible]







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KW Meningococcus B; MenB; ds.
XX
XX Neisseria meningitidis.
XX
XX WO200022430-A2.
XX
XX 20-APR-2000.
XX
XX 08-OCT-1999; 99WO-US23573.
XX
XX 09-OCT-1998; 98US-0103794.
XX
XX 30-APR-1999; 99US-0132068.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC,
XX Maignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
XX Rappuoli R, Pizza M;
XX
XX WPI: 2000-318079/27.
XX
XX Isolated nucleotide sequences of Neisseria meningitidis which can be
XX used in the diagnosis and treatment of N. meningitidis infection and
XX other Neisserial infections, for example, N.gonorrhoea
XX
XX Claim 7; Page 1396-1406; 1760pp; English.
XX
XX The present invention describes methods of obtaining immunogenic
XX proteins from Neisseria genomic sequences. AAA81453 to AAA82414
XX represent specifically claimed Neisseria meningitidis genomic DNA
XX sequences: AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
XX Neisseria DNA sequences and their corresponding proteins: AAA81254 to
XX AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
XX isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
XX AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
XX sequences, which are all used in the exemplification of the present
XX invention. The nucleic acid sequences, protein sequences, and antibodies
XX against them, can be used in the manufacture of a composition. The
XX composition can be used as a medicament (or in the manufacture of a
XX medicament) for treating, preventing or diagnosing infection due to
XX Neisserial bacteria. For example, some of the identified proteins could
XX be components of vaccines against Meningococcus B; against all serotypes;
XX and/or against all pathogenic Neisseriae. Identification of sequences
XX from the bacterium will also facilitate production of biological probes,
XX particularly organism-specific probes. Attempts to make efficacious
XX Meningococcus B vaccines have failed mainly due to antigen tolerance.
XX Multivalent vaccines have also been tried but none have successfully
XX overcome antigenic variability. The provision of further, complete
XX sequences may provide an opportunity to identify secreted or surface
XX exposed proteins that may be presumed targets for the immune system and
XX which are not antigenically variable or at least more conserved than
XX other more variable regions.
XX
XX Sequence 35133 BP; 8216 A; 9873 C; 8987 G; 8057 T; 0 other;
SQ
Query Match 1.0%; Score 43.4; DB 21; Length 35133;
Best Local Similarity 47.0%; Pred. No. 1.2;
Matches 134; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

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DB 3168 actataccatttgacacaaatacgcagcgactaccgcgagcgagagctccg 3227
OY 3864 cgggttttagcagcgagcgttttcagcagcgtcgagcgcaaa 3928
DB 3228 ccggtgaaccgcgcgcgctgtcgtcgagcgctgtccaaaa 3272
RESULT 43
ID AAF21611 standard; DNA: 349980 BP.
XX
XX AAF21611;
XX
XX 13-MAR-2001 (first entry)
XX
XX Neisseria meningitidis B nucleotide sequence SEQ ID NO:112.
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
XX diagnosis; antigen; detection; infection; gene therapy; antibacterial;
XX ds.
XX
XX Neisseria meningitidis.
XX
XX WO200066791-A1.
XX
XX 09-NOV-2000.
XX
XX 08-MAR-2000; 2000WO-US05928.
XX
XX 30-APR-1999; 99US-0132068.
XX
XX 08-OCT-1999; 99WO-US23573.
XX
XX 28-FEB-2000; 2000GB-0004695.
XX
XX (CHIR ) CHIRON CORP.
XX (GENO ) INST GENOMIC RES.
XX
XX Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC, Maignani V;
XX Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V,
XX Frazer CM, Grandi G;
XX
XX WPI: 2000-647603/62.
XX
XX Neisseria meningitidis B full length genome sequence and open reading
XX frames are used to detect, treat and prevent Neisserial infections -
XX
XX Claim 7; Appendix A; 692pp; English.
XX
XX The present invention describes the full length genome of
XX Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607
XX to AAF21613 represent fragments of the NMB genomic sequence, as the
XX sequence was too long to go in a record on its own it was split into 8
XX sequences which overlap each other at the beginning and end of each
XX sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at
XX the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated at
XX the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the
XX Neisseria proteins given in AAB58550 to AAB58593, and AAF21589 to
XX AAF21606 represent PCR primers which are used in the exemplification of
XX the present invention. The NMB genome and fragments from it have
XX antibacterial activity, and can be used in vaccines and gene therapy.
XX Neisseria nucleic acids, proteins and/or antibodies which binds to the
XX proteins can be used in compositions for treating or preventing infection
XX due to Neisserial bacteria or as a diagnostic reagent for detecting the
XX presence of Neisserial bacteria or of antibodies raised to Neisserial
XX bacteria. Computers, computer memory, computer storage medium or computer
XX databases can be used in a search to identify open reading frames (ORFs)
XX or coding sequences within the NMB genome. The DNA sequences provide
XX further opportunities to find antigenic or immunogenic proteins which are
XX more effective in vaccines than the outer membrane proteins currently
XX used.
XX
XX Sequence 349980 BP; 87189 A; 93501 C; 84627 G; 84663 T; 0 other;
SQ

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RESULT 44  
AAAB1489  
ID AAAB1489 standard; DNA; 837096 BP.  
XX  
AC  
XX AAAB1489;  
DT  
XX 04-DEC-2000 (first entry)  
DE N. meningitidis partial DNA sequence gnm\_37 SEQ ID NO:37.  
XX  
KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;  
XX antigen; vaccine; diagnosis; infection; antibacterial; identification;  
XX Meningococcus B; MenB; ds.  
XX  
OS Neisseria meningitidis.  
PN WO200022430-A2.  
PD 20-APR-2000.  
PP  
PF 08-OCT-1999; 99WO-US23573.  
PR 09-OCT-1998; 98US-0103794.  
PR 30-APR-1999; 99US-0132068.  
PA  
XX (CHIR ) CHIRON CORP.  
PI Frazer CM, Hickey E, Peterson J, Tettein H, Venter JC;  
PI Maignant V, Galeotti C, Mora M, Ratti G, Scarselli M, Scariato V,  
PI Rappunoli R, Pizsa M;  
DR WPI: 2000-318079/27.  
XX  
XX  
XX Isolated nucleotide sequences of Neisseria meningitidis which can be  
PT used in the diagnosis and treatment of N. meningitidis infection and  
PT other Neisserial infections, for example, N.gonorrhoea -  
PS  
XX Claim 7: Page 629-865; 1760pp; English.

The present invention describes methods of obtaining immunogenic CC proteins from Neisseria genomic sequences. AAA81453 to AAA82414 CC represent specifically claimed Neisseria meningitidis genomic DNA CC sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the CC isolation of Neisseria meningitidis DNA sequences; and AAA81322 to CC AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF

Query Match	1.08;	Score 43.4;	DB 21;	Length 837096;
Best Local Similarity	60.58;	Pred. No. 9.6;		
Matches 305;	Conservative 0;	Mismatches 196;	Indels 3;	Gaps 1

RESULT	45
AAA30290	
ID	AAA30290 standard; DNA; 3489 BP.

AC	AAA30290;	
XX		
DT	11-SEP-2000	(first entry)
XX		
DE	Kaposi's sarcoma-associated	herpesvirus LANA gene.
XX		
XX	Kaposi's sarcoma-associated	herpesvirus; KSHV; Rhadino virus
XX		

